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OM protein · protein search, using sw model

Run on:	October 31, 2002, 13:25:03; Search time 30 Seconds (without alignments) 2439.921 Million cell updates/300
Title:	9-841-553-1
Seguence:	343/ 1 MKRLGAVVLALVLVGLLAGTYAYSTYGWADYQLKAVVYYG 659
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	747574 seqs, 111073796 residues
Total number of	Total number of hits satisfying chosen parameters: 747574
Minimum DB seq.	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post.processing	Post-processing: Minimum Match 10% Maximum Match 100% Maximum Match 100% Listing first 45 summaries
Database :	A_Geneseq_032802:* 1: /SIDS1/gogdata/geneseq/geneseqp-emb1/AA1980.DAT:*

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3. Silbsily goddatalygeneseqyeenebly AA1981 DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being present and is derived by analysis of the total score distribution.

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SUMMARIES	Q ;	AAW24121	AAW94840	AAW24123	AAW24129	AAW94841	AAW24122	AAW94838	AAW94836	AAR87009	AAR87011	AAW24126
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18 0	Query	100.0	100.0	84.8	72.3	72.3	62.2	62.2	49.7	33.6	27.2	27.2
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Streptomyces viri	DhpA-mel chimeric	Fragment of dhpA	Transglutaminase	Pyrococcus protes	Sequence of modif	Keratinase from B	Dacillus lichenif	Amino acid sequen	Subtilisin useful	Bacillus carlsber	Bacillus amyloliq	Protease. Pyroco	Pyrococcus furios	MOSUSSESSES ID	Mutant subtilisin	COO2 mutant of the	Pro-subtilisin BP	Amino acid sequen	Sequence of alkall	Encodes subtilisin	Bactling amytoridu	DOTTOTAMB ENTITIES	Amino acid sequence	Subtiliain gene p	TOUR TOUR TOURS	B. cavlol forefactor	B. amyloliquefacte	Wild type subtili	Subtilisin BPN'.	Bacillus amylolig	B. amyloliquefacte	amy tot tidnetaction											tability; thermococcus celer.										Takakura H;			tre emposition the part	
AAW13667	AAWIJODG	AAW13000	AABB1180	AAWZ412/	AAR04137	AAR86521	AAW26762	AAW46598	AAW31600	AAR34251	AAY 7 7001	AAK8/008	42142WAA	TO DO	1420444	AAKTU401	AAMUUUA A	AAM40090	AAD2123	44070486	AAP70052	AAD90271	AAD02736	AARSAGI	AAR75161	AAR7 4223	AAR65247	AAR96237	AAR86876	AAY39228	AAY16767 AAY16769		ALIGNMENTS				659 AA.						thermal stabi										Morishits M,			oding them obtained	
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This sequence represents the protesse from Thermococcus celer DSM_2476. This sequence is a protesse of the invention. The protesses of the invention have extremely high thermal stability. The protesses can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                           LDLYLYDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLVYAXSTYGWADYQLKAVYYYG-659
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                                                                                                                                                                                                                                                                                                                                                                                              110.0%; Score 3437; DB 18; Length 659; Larity 100.0%; Pred. No. 2.1e-203; Conservative 0; Mismatches 0; Indels 0;
Claim 1; Page 82-85; 159pp; Japanese
                                                                                                                                        Similarity
                                                                                                     659 AA;
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Best Local Simi
Matches 659;
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the invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40-10-769-7 (optimum 80-95 deg-C), working ph 5-10 (optimum 6-8), and retains more than 90% of its activity after 8 hours at 95 deg.C. The invention giso provides gene sequences encoding a polypeptide of formula SIG-Ria-019-019-04-18-0-80. Where SIG is a signal peptide from subtilisin, and PRO is the above protease. Host cells especially Bacillus straigs transformed with vectors comprising the genes are used for the reconfunant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foodstuffs and for chemical synthesis.

659 AA;

Sequence

for

Recombinant hyperthermostable protease from Pyrococcus furiosus and gene encoding it, for large scale production of the protease industrial use.

Disclosure; Page 55-58; 82mp; Japanese.

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Takakura

Shimojo I,

Asada K, Kato I, Morishita M,

WPI; 1999-080907/07. N-PSDB; AAX05926.

(TAKI) TAKARA SHUZO CO LID

10-JUN-1997;

98WO-JP024 55 97JP-0151969

W09856926-A1

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GPNIYIVGSPAAASKVITWAAA WOSNDNIASFSSRGPTADGRIKPEVVAPGVDIIAPRASG 360
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                                                                   181 VIGWYDAVNGRSTPYDDOGMGPHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGS
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                                   1 MKRLGAVVLALVLVGLLAGIALAAPVKPVVRNNAVQQKNYGLLTPGLFKKVQRMNWNQEV
                                             (21 RVSGIKFIQEDYKVQVDDATSVSC. (GADTVWNSLGYDGSGVVVA.) VDTGIDANHPDI.KGK
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Score 3437; DB 20;
Pred. No. 2.1e-203;
Mlsmatches 0; 1
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Best Local Similarity 100.0%;
Matches 559; Conservative 0;
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nostable; protease; thermophilic; bacterium; subtilision drug; washing agent; foodstuff; chemical synthesis.

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AAW94840 standard; Protein; 659

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(first entry)

06-MAY-1999

AAW94840;

W09856926 Seq ID 12. Hyperthermostable; additive; drug; was Thermococcus celer

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SGGGNPNPNPNPNPTPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDLTFDTSYND
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84.8%; Score 2914; DB 18; Length 659;
Best Local Similarity 83.7%; Pred. No. 3e-171;
Matches 558; Conservative 47; Mismatches 46; Indele 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease; research reagent; thermal stability.
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Tsunasawa S, Yamamoto K;
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LGADGSGSVSTIIAGVDM,VQMKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV 292
                                       293 VCVAAGNSGPATTTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                           IIAPRASGTSMGTPIND/YTKASGTSMATPHVSGVGALILOAHPSWTPDKVKTALIETAD 412
                                                                                                                413 IVAPKBIADIAYGAGRVEVYHAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFYTATLY 472
                                                                                                                                                      473 WDTGSSDIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDV 532
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                                                                                                                                                                                                                                     This sequence represents the protesse from Pyrococcus furiosus DSM-3639.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Page 125-128, 173pp; Japanese.
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Tsunasawa S, Yamamoto K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIAPRASGTSWGTPINDYYTKASGTSNATPHVSGVGALILQAHPSWTPDKVKTALIETAL 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (111:11111) | 11111 | 1111 | 11111 | 1111: | 11 | 11111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGADGSGSVSTIIAGYDWYVONKDKYGIRVINLSLGSSQSSDGTDSLSGAVNNAWDALTY, 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTRVSGIKFIQEDYKVQVDDA----TSVSQ1GADTVMNSLGYDGSGVVVAIVDIG1DAN 17,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 KAKLSGVRFIGEDYKVTVSAELEGLDESAAQVAATVWN-LGYDGSG1TIGIIDTG1705$173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 HPDLKGKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGTGSV-NSQYIGVAPGAKLVGVKW 23,2
                               pe
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyperthermostable; protease; thermophilic; bacterium; subtil, sip; additive; drug; washing agent; foodstuff; chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 72.3%; Score 2483.5; DB 18; Length 654; Bost Local Similarity . 72.1%; Pred. No. 8.9e-145; Matches 481; Conservative 69; Wismatches 96; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hyperthermostable protesse.
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                                                                                                                                                                                  654 AA;
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                                                                                                                                                                                     Sequence
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AAW94841
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the invention relates to a hyperthermostable processe derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protesse has working temperature 40-110° deg.C (optimum 80-95 deg.C), working pub 5-10 vorking temperature at 19.10° deg.C (optimum 80-95 deg.C), working pub 5-10 publishmum 80-95 deg.C. The invention also provides gene sequences encoding a style formula SiG-hardy Asnr-Ro, where SiG is a signal polypeptide from subtilision, and PRO is the above processe. Host cells peptide from subtilision, and PRO is the above processe. Host cells (especially Bacillus strains) transformed with vectors comprising the genes are used for the recombinant production of the processe. The hyperthermostable protesse. Which can be prepared in quantity suitable hyperthermostable protess. Which can be additive for drugs, washing agents and foodstuffs and for chémical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 VVVAAGUSGPNKYIIGSPAAASKVIIVGAVDKYDVITSFSSRGPTADGRLKPEVVAPGNW 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIABRASGISMGTPINIG TKANGISMATPHVSGVGALILQAHPSWTPDKVKTALIETAD 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVAPKETADIAYGAGRATAYKA KYDDYAKLIFTGSVADKGSATHIFDVSGATFYTATLY 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 EVDTVIMEGSYGDRDRAVKŲL?LMGAQVKYSYKIIPAVAVKIKARDLLLTAGMIDTGYFG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant hyperthermostable protesse from Pyrococcus furiosus and gene encoding it, for large scale production of the protesse for industrial use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 YCVAAGNSGPNIYIYGSPA-A-A-TIYGAVDSNDNIASFSSRGPTADGRIKPBYYAPGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGADGSGSVSTIIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAMDAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPDLKGKYIGWYDAVNGRSTPYDDQGHGTHYAGIVAGTGSV-NSQYIGVAPGAKLVGVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKRIGAVVLALVLUGLLAGTAJAADVKPV - - VRNHAVQQKNYGLLTPGLFKKVQRMNWNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.5%; Score 2483.5; DB 20; Lengt: Best Local Similarity 72.4%; Pred. No. 8.99-145; Matches 481; Conservative 65; Hismatches 96; Indels
                                                                                                                                                                    Takakura
                                                                                                                                                                        Shimojo
                                                                                                                                                                                                                                                                                                   Disclosure; Page 60-63; 82pp; Japanese.
                                                                                                                                                                         Kato I, Morishita M.
                                                                                                                                          (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                97JP-0151969
                                                                                                                                                                                                    WPI; 1999-080907/07.
N-PSDB; AAX05929.
Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 AA;
                                                                                                                 10-JUN-1997;
                            W09856926-A1
                                                         17-DEC-1998
                                                                                                                                                                              Asada K,
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This sequence represents the protease from Pyrococcus furiosus DSM-3638. This sequence is a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
593 TFDTSYNDLDLYLYDPNGNLVDRSTSSNSYBHVEYANPAPGTWTFLVYAYSTYGNADYQL 652
                                                       533 VSDGSLSQSGGGNPNPNPNPNPNPTTDTQTFTGSVNDYWDTSDTFTMNVNSCATKITGDL, 592
                                                                    533 VSDGSLSQ-----PGSSPSPQPEPTVDAKTFQGSDHYYYDRSDTFTMTVNSGATKITGDL, 587
                                                                                                                                Protease; research reagent; thermal stability; pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and areuseful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.2%; Score 2138.5; DB 18; Lengt. Best Local Similarity 78.3%; Pred. No. 1.1e-123; Matches 407; Conservative 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asada K, Kato I, Mitta M, Morishita M, Takakura
Tsunasawa S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label = Gly, val
/note = "encoded by GNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 87-90; 159pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
Misc-difference 428
                                                                                                                                                                                                                                                                           AAW24122 standard; Protein; 522 AA
                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furiosus protease.
                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus furiosus DSM-3638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-JP03253,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95JP-0323285.
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                                                                                                                                                                                                                                                                                                                                  20-APR-1998 (flrst entry)
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N-PSDB; AAT85668.
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                                                                                                                                                                       653 KAVVYYG 659
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                                                                                                                                                                     320 GAVDSNDNIASESSRGPTALGELKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTSM 379
                                                                                                                                                                                                                                        380 ATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYKAIKYDD 439
                                                                                                                                                                                                                                                          500 YGFEKVGYYNPTAGTWTVXVYSYKGAANYQVDVVSDGSLSQSGGNPNPNPNPNPTPTTD 559
                                                                                                                                                                                                                                                                                                                                                                                                                                               560 TOTFTGSVNDYNDTSDTFTMNVMSGATKITGDLTFDTSYNDLDLYLYDDNGNLVDRSTSS 619
9 SAAQVMATYVWN-LGYDGSGEFIGIIDIGIDASHPDLQGKVIGWVDFVNGRSYPYDDHGH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant hyperthermos and protesse from Pyrococcus furiosus and gene encoding it, for inrge scale production of the protesse for industrial use.
                                   201 GTHVAGIVAGTGSV-NSOYYGYAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVONKDKYG
                                                                                                                                                                                                                                                                                                           440 YAKLIFIGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEVDYSYTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyperthermostable; protesse; thermophilic; bacterium; subtilisin; additive; drug; washing sgent; foodstuff; chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takakura H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSYEHVEYANPAPGTWT#LVYXATSTYGWADYQLKAVVYYG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimojo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Wealiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW94838 standard; Protein; 522 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asada K, Kato I, Morishita M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 428
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Claim 1; Page 39-41; 62pp; Japanese.

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DB 18; Length 522;

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141 SVSQIGADTVWASLGYDGSGVVVALVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 200

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The invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protesse has working temperature 40-10 deg-C (optimum 80-95 deg-C), working pF 5;10 (optimum 6-8), and retains more than 90% of its activity after 8 hours at 95 deg-C. The invention also provides gene sequences encoding a polypeptide of formula SiG-Ala-Gly-Gly-Asn-PRO, where SiG is a signal peptide from subtilisin, and PRO is the above protease. Host cells (especially Bacillus Strains) transformed with vectors comprising me genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foodstuffs and for chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAYDSNDNIASFSSRGPTADGRLKPEVYAPGYDIIAPRASGTSMGTPINDYYTKASGTSM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGFEKVGYYNPTAGTWTVKVVSTKGAANYQVDVVSDGSLSQSGGGNPNPNPNPTP?" 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGFEKVGYYNPTDGTWTIKVVSYSGSANXQVDVVSDGSLSQ-----PGSSPSPQFEPTVD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 TOTETGSVNDYWDTSDTFTMNVNSGATKIIGDLIFDTSYNDLDLYLYDPNGNLVDRSTES; 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPHVSGVGALILOAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYKAIKKDD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTHVAGIVAGTGSV-NSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVONKDKYG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAKLIPTGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEVDYSYTAY 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                68 GTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIKGVEMAVDNKDKYG 127
                                                                                                                                                                                                                                                                              Query Match 62.2%; Score 2138.5; DB 20; Length 522; Best Local Similarity 78.3%; Pred. No. 1.1e-123; Matches 407; Conservative 36; Mismatches 70; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                          NSYEHVEYANPAPGTWTFLVYAYSTYGWADYQLKAVVYYG 659
                                                                                                                                                                                                                                                   522 AA;
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
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AAR87009 standard; Protein; 237

RESULT 9
AAR87009
ID AAR8
XX
AC AAR8

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The invention relates to:a h.perthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40.10 dec ( optimum 6.95 deg.C.), working pH 5.10 (optimum 6.95 deg.C.), working pH 5.10 (optimum 6.95), and retains more than 90% of its activity after 8 hours act 95 deg.C. The invention also provides gene sequences encoding a polypeptide of formula SiG-Ala-Gly-Gly-Asn-PRO, where SiG is a signal peptide from subtilisin, and RDO is the above protease. Host cells (especially Bacillus) transformed with vectors comprising the genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foodstuffs and for chamical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 GAVDSNDNIASESSRGPTAEGREKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTSM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 SVSQIGADTVWNSLGYDGRGYVYATVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 IRVINLSLGSSQSSDGTDSESQAVNNAMDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 GAVDKYDVITSFSSRGPTAFGRIKPEVVAPGNWIIAARASGTSMGQPINDYYTAAPGTSM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 ATPHVSGVGALILQAHPSW/PONTYKTALIETADIVAPKETADIAYGAGRVNVYKAIKYDD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 YAKLIFIGSVADKGSATHIF TO FIAIFVIATLYHDIGSSDIDLYLYDPNGNEVDYSYTAY 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant hyporthermostable protesse from Pyrococcus furiosus - and gene encoding it, for large scale production of the protesse for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 SAAQVMATYWN-LGYDGSGTTJSIIDTGIDASHPDLQGKYJGWVDFVNGRSYPYDDIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GTHVAGIVAGTGSV-NSQYTEVAFGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
                                                                                                                                                            Takakura H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 YGPEKVGYYNPTDGTWTIKVVVSSGSANYQVDVVSDGSLSQPG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.74; Score 1707; DB 20;
llarity 80.6%; Pred. No. 2.9e-97;
Conservative (29; Mismatches 47;
                                                                                                                                                         Ė
                                                                                                                                                              Shimojo
                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 35-37; 82pp; Capanese.
                                                                                                                                                              Mortshirs M.
                                                                           97JP-0151969.
                                     98WO-JP02455.
                                                                                                                    (TAKI ) TAKARA SHUZO CO LED.
                                                                                                                                                                                               WPI; 1999-080907/07.
N-PSDB; AAX05920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
frocal Similarity
                                                                                                                                                            Asada K, Kato I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 412 AA;
                                                                                                                                                                                                                                                                                                           industrial use.
                                                                           10-JUN-1997;
                                   04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 325;
17-DEC-1998
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200 HGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYG 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 IRVINESLGSSQSSDQADSESSOANNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus hyper: thermostable protesse gene · useful for recombinant prodn. of hyper:thermostable protesse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; research reageing thermal stability; thermococcus celer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Invention relates to a gene (AAT08141) that codes for a hypertramostable protess: (AAR87007) of Pyrococcus furiosus. 2 DNn sequences (AAT08135-24) are provided encoding peptides (AAR87010-11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
27.25; Score 935; DB 17; Length 188; Best Local Similarity 98.44; Pred, No. 3.36-50; Matches 184; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                 Tsunasawa
               Protease; hyperthermostable; thermostability
                                                                                                                                                                                                                                                                            Asada K, Kato I, Mitts M. Norishita M,
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 66-67; 85pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24126 standard; Protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermococcus protease fragment.
                                                                                                                                                                                       94JP-0173913.
                                                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO - CD.
                                                                                                                                                     95WO-JP01095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-1996, 96WO-JP03233
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                                               Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                             WPI; 1996-049674/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 ATPHVSG 386
                                                                                                                                                                                     26-JUL-1994;
13-JUN-1994;
                                                                                409534645-A1
                                                                                                                                                     05-JUN-1995;
                                                                                                                  21-DEC-1995,
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                                                                                                                                                                                                                                                                                           Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW24126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 DEKGKVIGWYDAVNGRSTPYDDQCHGTHVAGIVAGTGSVNSQYIGVABGAKLVGVKVLGA 235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 DGSGSVSTIIAGVDWVVQNKDKYGIRVINLSLGSSOSSDGTDSLSQAVNNAWDAGIVVCV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DOSGSVSTIIAGVDWVVONKDKTGIRVINLESLGSSGSSDGTDSLSQAVNNAWDAGIAVCV, 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DLKGKVIGHYDAVNGRSTPYDDQCHGTHVAGIVAGTGSVNSQYIGVAFGAKLVGVKVGG, 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Invention relates to the hyperthermostable protesse of Pyrococous furiosus and its prodn. as a recombinant protein in transformants using a vector carrying the protesse gene (AATOB141). A genomic DNA sequence of the invention is given in AATOB131 and its encoded protein in AAR87009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Natch 33.6%; Score 1154; DB 17; Length 237; Best Local Similarity 97.4%; Pred. No. 1.5e-63; Matches 224; Conservative 1; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 PRASGTSMGTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morishita M, Tsunasawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus hyper:thermostable protease gene
recombinant prodn. of hyper:thermostable protease
                                                                                                                                                                            /note= "unspecified amino acid"
                                                                      Protease; hyperthermostable; thermostability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 70-71; 85pp; Japanese.
                                                                                                                                    Location/Qualiflers
Misc-difference 196
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                                                                                                                                                                                                                                                                                                                                                                                                          Asada K, Kato I, Mitta M,
Yamamoto K;
                                                                                                                                                                                                                                                                                   95WO-JP01095
                                                                                                                                                                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                                     94JP-0130236
                                                                                                                                                                                                                                                                                                                    94JP-0173912
                                  Hyperthermostable protease.
   10-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-049674/05.
                                                                                                         Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 237 AA;
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Peptide sequence

AAR87011;

AAR87011 ID AAR XX AC AAR XX IO-XX IO-XX DE PEE

RESULT 10

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N-PSDB; AAT08131.

×44×44×4×0000×0

35-JUN-1995;

W09534645-A1 21-DEC-1995

13-JUN-1994; 26-JUL-1994;

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Nakashima

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This sequence is an asymmetric hydrolase encoded by the Streptomyces viridosporus dhpA gene. The enzyme acts on 4-substituted-1,4-dihydropyridine derivatives. The enzyme allows the efficient conversion of 4-substituted-1,4-dihydropyridine esters to chiral partially hydrolysed derivatives, i.e. use in the symbhesis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 ASGISMATPHVSGVGALILOÄHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGTHVAGIVAGTGSVN-SQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDMVVQNKDKY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 GIRVINLSLGSSQSSDGTDSLSQAVNN-AWDAGIVVCVAAGNSGPNTYTVGSPAAASKVI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVGAVDSNDNIASFSSRGP-TADGRLKPEVVAPGVDIIAPRASGTSMGTPIND---YYTK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 TVCAVDDKDKLADFSSTGFRLGBGAIKPDVTAPGVDITAASAEGNDIGQEVGEGPAGYMT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 LPADAARLVASGKIDRRLFDITELG--KAATRNSQKQGLKVIV---GYQGAARAKAEVR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALQQTVIADPYSVSFOVROPHT: DEPVTKQLTYRNLGTQDVTLKLTSTATDPKGKAAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEDVSGATEVTATLYWDTGS&DIOLYLYDPNGNEVDYSYTAYYGFBKVGYYNPTAGTWTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFFTLGATTVTVPA---G:SASYDWTADTRLGGTVDGAYSAYVVATGGGQTVRTAAAVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 KVVSY-----KGARINQVDVVSDGSLSQSGGNPNPNPNPNPTPTTDTQTF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGS-VNDYWDTSDTFTM-....-NVNSGATKITGDLTFDT-SYNDLDLYLYDPNGNLV
                                                                                                                                                                                                  Asymmetric hydrolase gene derived from Streptomyces viridosporus acts on 4-substituted 1,4-di.hydro:pyridine derivatives to produce chiral derivatives useful for synthesis of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 EVESYDVTVRHIGRDGKPTFFFTDLIGYAGLGSGRGYG-----APATDTATLRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 LAAPVKPVVRNNAVQQKNYG;LUPGLEKKVQRMNWNQEVDTVIMFGSYGDRDRAVKVLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 MGAQVKYSYKIIPAVAVKIKARELLIAGMIDTGYFGNTRVSGIKFIQEDYKVQVDDATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 EAGELRRILISLNADAVRIPHES --- ASELWDAVINGDRIASGIAHVWLDGVRRAALDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 VSQIGADIVWNSLGYDGSGVVVALVDIGIDANHPDLKGKVIGWYDAVNGRSTP--YDDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 665; DB 18;
Pred. No. 7.1e-33;
34; Mismatches 269;
                                                                                         Matsufuji M,
                                                                                                                                                                                                                                                                               Claim 3; Page 49-55; 78pp; Japanese
                                                                               zashiki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%
96JP-0067479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 31.28
Matches 216; Conservative
                                                      (SAOC ) MERCIAN CORP.
                                                                                                                                              WPI; 1997-145682/13.
N-PSDB; AAT61454
                                                                                           Artsawa A, Dobashi
Tsuruta T, Yoshioka
                                                                                                                                                                                                                                                                                                                                                                                                                                                              734 AA;
  29-FEB-1996;
31-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                  This sequence represents a fragment of the protease from Thermococcus celer DSM-2416 (see AAW24121 for full length sequence). This sequence is a fragment of the protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                               are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDMYVQNKDKYG 259°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 IRVINLSLGSSQSSDGADSLSGAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTSM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 IRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVYCVAAGNSGPNTYTVGSPAAASKVITV
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205..724
/note= "fragment of dhpA protein; see AAW13666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                             Protease(s) and genes encoding them obtained from Thermococcus Pyrococcus strains - have extremely high thermal stability and useful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                   Morishita M. Takakura H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
27.2%; Score 935; DB 18;
Best Local Similarity 98.4%; Pred. No. 3.3e-50;
Matches 184; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces viridosporus dhpA gene product.
                                                                                                                                                                                                                                                                                        Disclosure; Page 110-112; 159pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW13667 standard; Protein; 734 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-JP02147
                                                                                                   Asada K, Kato I, Mitta M,
Tsunasawa S, Yamamoto K;
                              95JP-0323285
                                                                (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces viridosporus.
                                                                                                                                                            1997-332794/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT85676.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asymmetric hyderive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-1996;
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                              12-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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26;

Length 734;

517

613

us-09-841-553-1.rag

141

82 MGAQVKYSYKIIPAVAVK,IKARBLLLIAGMIDTGYFGNTRVSGIKFIQEDYKVQVDDATS

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This sequence is a fusion protein comprising Streptomyces viridosporus dppA gene product (an asymmetric hydrolase) which acts on 4-substituted-1,4-dhydropyridine derivatives, and melanin from S. antibioticue. The blpA enzyme allows the efficient conversion of 4-substituted-1,4-dhydropyridine esters to chiral partially hydrolysed derivatives for use in the synthesis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart disease.
                                                                                                                                                                                                                                                                                                                      663 KGTYLVDSWIAKDFGTLKGGIDWLVQPKLSVTKDT-TLTLDARTIKAADITVFDPK---<sub>6</sub> 717
                                                                                                                                                                                DhpA-mel chimeric protein.

asymmetric hydrolase; dhpA; 4-substituted-1,4-dihydropyridine;
derivative; Streptomyces viridosporus; ester; chiral; synthasis;
cardiovascular; treatment; hypertension; ischaemic heart disease.
Chimeric Streptomyces viridosporus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%: Score 665; DB 18; Length 823;
31.2%; Pred. No. 8.2e-33;
Live 84; Mismatches 269; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asymmetric hydrolase gene derived from Streptomyces viridosporus -
acts on 4-substituted-1,4-d1:hydro:pyridine derivatives to produce.
chiral derivatives useful for synthesis of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arisawa A, Dobashi K, Isshiki K, Matsufuji M, Nakashima T;
Tsuruta T, Yoshioka T;
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1.34
1.134
1.254
205.724
205.724
70.te**see AAW13666*
735.484
700.te**melanin (partial sequence)*
                          614 DRSTSSNSYEHVEYANPAPGTWTFLVXAYSTYG 646
                                           AAW13668 standard; Protein; 823 AA.
                                                                                                                                                                                                                                                                  Chimeric Streptomyces viridosporus. Chimeric Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 37-43; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0067478
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N-PSDB; AAT61455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         823 AA;
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31-JUL-1995;
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                                                                                                                                           AAW13668;
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                                                                                          RESULT 13
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ID AAW1
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142 VSQIGADTVHNSLGYDGSGYVVAIVDTGIDANHPDLKGKVIGMYDAVNGRSTP--YDDOG 199
                                                                                                                                                                   HGTHVAGIVAGTGSVN-SGRIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVONKDKY 258
                                                                                                                                                                                                     259 GIRVINLSLGSSQSSDGTDSLEQAVNN-AWDAGIVVCVAAGNSCPNTYTVGSPAAASKVI 317
                                                                                                                                                                                                                                                                                                       318 TVGAVDSNDNIASFSSRG2-TADGRLKPBVVAPGVDIIAPRASGTSMGTPIND---YYTK 373
                                                                                                                                                                                                                                                                                                                                                                                                        434 AIK----YDDYAKLTFTGSVADKGSATH 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 ALGOTVIADPVSVSFGVGGWPHTDDEPVTKOLTYRNLGTGÖVTLKLTSTATDPKGKAAPA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 KGTYLVDSWIAKDEGTLKGGTDWLVQPKLSVTKDT-TLTLDARTTKAADITVPDPK---- 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 TGS-VNDYWDTSDTFTM----NVNSGATKITGDLTFDT-SYNDLDLYLYDPNGNLV 613
152 EAGELRRTITSLNADAVRTPHED---ASELWDAVINGDRIASGIAHVWLDGVRRAALDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 ASGTSMATPHVSGVGALILQAHFSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 TFDVSGATFVYATLYMDTGSSDIDLYLYDPNGNEVDKSYTALYGFBKVGYYNPTAGTWTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 KVVSY-----KGA-WAKQVDVVSDGSLSQSGGANPNPNPNPNPNPTDTDTGTF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asymmetric hydrolase; dhpa; 4-substituted-1,4-dihydropyridine; derivative; Streptomyces viridosporus; ester; chiral; synthesis; cardiovascular; treatment; hypertension; ischaemic heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 DRSTSSASYEHVEYANPAPCTNTFLVYAYSTYG 646
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Misc-difference 29
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LAPADARLVASCKLDRRLFDITELG--KAATRNSQKGGLKVIV--GYGGAARAKAEVR:15:

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22 LAAPVKPYYRNNAVQQKNYGLLTPGLFKKYQRMNHNQEVDTVINFGSYGDRDRAVKVIRL 81.

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AAB81180;
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                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                         This sequence is a fragment of an asymmetric hydrolase which acts on 4-substituted-1,4-dihydropyridine derivatives. The DNA sequence encoding the hydrolase (DhpA) was isolated from the chromsonal DNA of Streptomyces viridosporus. The enzyme allows the efficient conversion of 4-substituted-1,4-dihydropyridine esters to chiral partially mydrolysed derivatives, for use in the synthesis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 DKALQOTVIADPVSVSFGVQQMPHTDDEPVTKOLTYRNLGTQDVTLKLTSTATDPKCKAÄ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THIFDVSGAIFVTAILYWDIGSSDIDLYLYDPNGNEYDYSYIAYYGFEKVGYYNPTAGIW 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 PAGFFILGAITVIVPA---GGSASVDMTADTRLGGTVDGAYSAYVVAIGGGGTVRIAAAY 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 TVKVVSY------KGAANYQVDVVSDGSLSQSGGGNPNPNPNPNPTPTTDTQTF- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 OREVESYDVTVRHIGRDGKPTTEHLIDLIGYAGLGSGRCYG-----APATDTATLR 453
                                                                                                                                                                                                                                                                                                                                             432 YKAIK-----YDDYAKLIFTGSVADKGSA #55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 TKASGTSWATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKELADIAVGAGRVN7 433
                                                                                                                                                                                                                                                                                                                                                                                          140 TSYSOIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTP- 75D 197
                                                                                                                                                                                                                                                                                                                                                                                                                                            198 OCHCTHVAGIVAGTGSVN-SQIIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQKKD:256
                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 KYGIRVINLSLGSSQSSDGTDSLSQAVNN-AMDAGIVVCVAAGNSGPNTYIVGSPAANSK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.8%; Score 647.5; DB 18; Length 520; 35.9%; Pred. No. 5.5e-32; vative 58; Mismatches 177; Indels 85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 VITYGAVDSNDNIASFSSRGP-TADGRLKPEVVAPGVDLIAFRASGTSMGTPIND---YX
                                                                                                                                     Asymmetric hydrolase gene derived from Streptomyces viridosporus acts on 4-substituted-1,4-d1:hydro:pyridine derivatives to produce chiral derivatives useful for synthesis of cardiovascular drugs
                                                                   Nakashima T;
                                                                      Matsufuji M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB81180 standard; Protein; 1079 AA.
                                                                                                                                                                                             Claim 1; Page 60-63; 78pp; Japanese.
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                                                                        Isshiki
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.94 tos 179; Conservative
                                                                        Arisawa A, Dobashi K,
Tsuruta T, Yoshioka T;
                                                 (SAOC ) MERCIAN CORP.
                                                                                                             WPI; 1997-145682/13.
N-PSDB; AAT61454-55.
                                                                                                                                                                                                                                                                                                                                  520 AA;
                  29-FEB-1996;
31-JUL-1995;
                                                                                                                                                                                                                                                                                                                                     Seguence
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AAB81180
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This invention relates to a process for the production of a foreign secretory protein through the construction of a recombinant coryneform secretory protein through the construction of a recombinant coryneform becterium. The coryneform becterium is transformed with an expression construct in which DNA encoding a target foreign protein pro-structure is ligated to the downstream region of DNA encoding the signal peptide algoriant the vector, the bacterium is cultured, and the pro-peptide cleaved from the vector and expressed protein. Transglutaminases produced using this process are useful in the food processing and pharmaceutical industries. The present useful in the food processing and pharmaceutical industries. The present used in examples illigizating the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -IETADIVAPKEIADIAYGRURAVKAIKY--------DD---YAKLT 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Efficient secretory production of foreign proteins e.g. transglutaminase employing transformant coryneform bacterium, simply industrial scale with directirecovery for use in food processing and pharmaceutical industry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 DLKGQYTA---SKNFTSAPTFGERVGHGHVABIAAGTGAGSKGTYKGVAPGAKILNGKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.5v. Score 636; DB 22; Length 1079; Best Local Similarity 32.24 Pred. No. 6.9e-31; Additional 201; Conservative 72; Mismatches 219; Indels 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsui H;
                                                                                 Coryneform bacterla; transglutaminase; food processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date M, Umezawa Y, Yokoyama K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 113-120; 151pp; Japanese.
                                       Transglutaminase related protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                    (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                           30-SEP-1999; 99JP-0280098
28-JUN-2000; 2000JP-0194043.
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                                                                                                                                            Streptomyces albogriseolus.
(first entry)
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  13-JUL-2001
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Search completed: October 31, 2002, 13:29:40 Job time : 34 secs

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OM protein · protein search, using sw model

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October 31, 2002, 13:28:38 ; Search time 13 Seconds (without alignments) 1238:190 Million cell updates/sec

Title: Perfect score:

US-09-841-553-1 3437 1 MKRLGAVVLALVLVGLLAGT......YAYSTYGWADYQLKAVVVYG 659 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

Total number of hits satisfying chosen parameters: 231628 segs, 24425594 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/prodata/1/18a/5A_COMB.pep:# /cgn2_6/prodata/1/18a/5B_COMB.pep:# /cgn2_6/prodata/1/18a/6A_COMB.pep:# /cgn2_6/prodata/1/18a/Re_COMB.pep:# /cgn2_6/prodata/1/18a/PcTUS_COMB.pep /cgn2_6/prodata/1/18a/PcTUS_COMB.pep Issued_Patents_AA: Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	, , , , , , , , , , , , , , , , , , , ,	Sequence 1, Appli				-	4 .	7	4	H	28		ì	v	č	~	-	Sequence 1 April		ì	- 3	Ä	4	6	Sequence 3, Appl1		: -	r		Judy Page April	ednonce	Pacent No. 4 126-55
		OI B	A 172-08-004-0107		77-77-8-60-60 - 00 +	C-RATA-AKB-BC		4 05-09-445-472-16	4 US-08-894-818B-3	472	4 119-00-445-477-4	T - 2 / 5 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 -	BT-750-06/-00-50	4 -02-000-60-S	ns-09-000-016-2	US-09-000-018-7	1 113-08-68-71	7-77-000 00 00	03-07-323-260A-4	US-08-845-295A-1	US-09-140-933-1	US-09-146-661-1	US-09-140-87	1-CTC 007 (0 0)	4 CC - 4 C - 10 CC	9.750-00-50-50- 116-00-00-00-01	SPECTO STORES	- 04 - 40 -	-07-923-260A	-03-52	445-47	178-155	,	
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ALIGNMENTS

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APPLICANT: MORISHITA, MISACE
APPLICANT: MANAMOTO, Katculiko
APPLICANT: ASADA, KIYOZC
APPLICANT: TSUNASAMA, SUNGUL
APPLICANT: ASADA, KIYOZC
APPLICANT: ASADA
ANDESSES: Browdy and Neimerk
STREET: Washington
STATE: Duited States of America Sequence 1, Application US/08894818B Patent No. 6261822 GENERAL INFORMATION: TELEFAX: (202) 628-5367 TELEFAX: (202) 737-3528 SEQUENCE CHARCTERISTICS: LENGTH: 659 anino acide STRANDEDNESS: 810-1 REFERENCE/DOCKET NUMBER FA

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GENERAL INFORMATION:
APPLICANT: TAKAKUKA, HIKATU
APPLICANT: SHIMONO, TOMOKO
APPLICANT: SHIMONO, TOMOKO
APPLICANT: SHIMONO, TOMOKO
APPLICANT: RATO, IKUNOSHIM
APPLICANT: RATO, IKUNOSHIM
FILE REPERENCE: TAKAKURA-6
CURRENT APPLICATION WUMBER: US/09/445,472
CURRENT APPLICATION WUMBER: 1999-12-06
PRIOR APPLICATION WUMBER: 151969/1997
PRIOR PILING DATE: 1997-06-10
                           Length 659;
                                                   Indels
                             ; Score 3437; DB 4;
; Pred, No. 6.7e-237;
0; Mismatches 0;
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Patent No. 6358726
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SOFTWARE: Patentin version 3.0
NEQ ID NO 12
LENGTH: 659
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APPLICANT: KATO, IKunoshin
TITLE OF INVENTION: HTFERTHADMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: "42
                            Indels
   Query Match 100.0%; Score 3437; DB 4; Best Incel Similarity 100.0%; Pred. No. 6.7e-237; Matches 659; Conservative C, Mismatches 0; Matches 659; Conservative C, Mismatches 0;
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419 Seventh Street N.W., Ste.
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Patent No. 6261822
GENERAL INFORMAT
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APPLICANT: TAKAKURA, HIKATU
APPLICANT: MORISHITA, MIK
APPLICANT: YAMAMOTO, KRIESZNYO
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STATE: D.C.
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ASADA, Klyozo
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83.7%; Pred. No. 1.1e-199;
Live 47; Mismatches 46; Indels 16
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fatentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/894,818B
FILING DATE: 20-WAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: PCT/JP96/03253
APPLICATION NUMBER: DT/JP96/03253
APPLICATION NUMBER: US 323285/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 84.8% Best Local Similarity 83.7% Matches 558; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide
US-08-894-8188-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293
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59 EVDTVIMEGSYGDRDRAVYVLR: HGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.3%; Score 2483.5; DB 4; Length Best Local Similarity 72.1%; Pred. No. 5.1g-169; Matches 481; Conservative 59; Nismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KATO, Ikunobhin
TITLE OF INVENTION: HYPEPTHERMOSTABLE PROTEASE GENES
HUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy, and Nelmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC CONGRIDE
CONFUTER: IBM FC CONGRIDE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: [%/08/894,818B
FILING DATE: 20-MAY 1996
CLASSIFICATION A 435
PRIOR APPLICATION NUMBER: [%/17/1996/03253
FILING DATE: 07-MOV-1996
APPLICATION NUMBER: [%/17/1996/03253
PRIOR APPLICATION DATA:
APPLICATION NUMBER: [%/17/1996/03253
APPLICATION NUMBER: [%/17/1996/03253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08: Browdy and Neimark
419 Seventh Street N.W., Ste. 300
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FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                        Sequence 35, Application US/06894818B
Patent No. 6561812
Patent INFORMATION:
APPLICANT: TAKAKURA, HIKATU
                                                                                                                                                                                                                                                                                                                          APPLICANT: TAKAKURA, HIKATU
APPLICANT: MORISHITA, MIO
APPLICANT: YAMAMOTO, KUTSUHIKO
APPLICANT: MITTA, MASAMOTI
APPLICANT: ASADA, KIYOZO
APPLICANT: TSUNASAWA, SISUMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Browdy, Roger L. REGISTRAIN NUMBER: 35.518
REFERENCE/DOCKET NUMBER: TATELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 654 pm:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide
US-08-894-818B-35
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STATE: D.C.
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US-08-894-818B-3
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
12.3%; Score 2483.5; DB 4; Length 654;
Best Local Similarity 72.1%; Pred. No. 5.1e-169;
Matches 481; Conservative 69; Mismatches 96; Indels 21; Gaps.
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                                                                              353 IIAPRASGISMGTPINDYYIKASGISMATPHVSGVGALILQAHPSWIPDKVKIALIETAD 412
                                                                                                                                                                                                                                                                        IVAPKEIADIAYGAGRVNVYKAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLY 472
                                                           HPDLKGKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGTGSV-NSQYIGVAPGAKLVGVKV 232
                                                                                                                              VCVAAGNSGPNITIVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                 233 LGADGSGSVSTIIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV 297
    119 NTRVSGIKFIQEDYKVQVDDA-----TSVSQIGADTVWNSLGYDGSGVVVAIVDIGIDAN 17,3
                       533 VSDGSLSQSGGGNPNPNPNPTPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09445472

| Patent No. 6358726
| Patent No. 6358726
| GENERAL INFORMATION:
| APPLICANT: TAXAKURA, Hikaru
| APPLICANT: HIMOJO, TOMOKO
| APPLICANT: SHIMOJO, TOMOKO
| APPLICANT: ASADA, KIYOZO
| STILE REFERENCE: TAXAKURA-6
| CURRENT FALING DATE: 1999-12-06
| CURRENT FILING DATE: 1999-12-06
| PRIOR APPLICATION NUMBER: 151969/1997
| PRIOR FILING DATE: 1997-06-10
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: PATENTIN VERSION 3.0
| SEQ ID NO 16
| LIFERTH AND 16
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| 648 TAKVYYG 654
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533 VSDGSLSQSGGNPNPNPNPNPNPTPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDL 592
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                                                                                                                                                                                                                                                                                                                                                                                                    292
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                                              119 NTRVSGIKFIQEDYKVQVDDA ****-TSVSQIGADTVWNSLGYDGSGVVVALVDTGIDAN 173
                                                                    232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 TFDISYNDLDLYLYDPNGRLÚÖRRTSSNSYEHVEYANPAPGTWTFLVYAYSTYGWADYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 VCVAAGNSGPNTYTVGSPAAASKYITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD
                                                                                                                                                                                                                                                                       174 HPDLKGKVIGWYDAVNGRSTRYÜDGGHGTHVAGIVAGTGSV-NSQYIGVAPGAKLVGVKV
                                                                                                                                      353 IIAPRASGTSMGTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETAD
LGADGSGSVSTITAGVDWVVQRKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KATO, Ikunoshia
TILLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compa:lble
OPERATING SYSTEM: PC-D>3/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Browdy and Felmark
STREET: 419 Seventh Street N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States & 2 America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/U8894818B Patent No. 6261822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TAKAKURA, HINJEL
APPLICANT: MORISHITA, MIS
APPLICANT: MORISHITA, MASONICA
APPLICANT: MITTA, MASONICA
APPLICANT: ASANA, KIVEN
APPLICANT: ASANA, KIVEN
APPLICANT: KATO, IKUNOSHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
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MORISHITA,

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APPLICANT: SIMUACO, TORORIO
APPLICANT: SIMUACO, TORORIO
APPLICANT: ASADA, KIYOZ;
APPLICANT: ASADA, KIYOZ;
APPLICANT: KATO, MOGGALIA
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
TITLE OF INVENTION: SYSTEM FOR
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION $:0
SEQ ID NO 4
LENGTH: 522
                                                                                                                                                                                                                      NAMEKEY misc_feature

: LOCATION: (428)..(428)

: OTHER INFORMATION: Xaa at position 428 is Gly or Val.

US-09-445-472-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 ATPHVSGVGALICQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYKAIRYDD 439
                                                                                                                                                                                                                                                                                                                                                      141 SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 200
                                                                                                                                                                                                                                                                                                         Query Match
62.2%; Score 2138.5; DB 4; Length 522;
Bast Local Similarity 78.3%; Pred. No. 1.4e-144;
Matches 407; Conservative 35; Mismatches 70; Indels 7; Gape
                                                                                                                                                                                                                                                                                                                                                                                                260 IRVINLSLGSSGSSDGTDSLSGAVNNAMDAGIVVCVAAGNSCPNTYTVGSPAAASKVITV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 IKVINLSLGSSQSSDGTDALSQAVNAANDAGLVVVVAAGHSGPHKYILGSPAAASKVITV.187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 GAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTSH 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDVVSDGSLSQSGGGNPNPNPNPNPTPTTD 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: /note= xaa at position 428 18 Gly or Val
US-08-894-8188-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     620 NSYEKVEYANPAPGTWTFLVYAYSTYGWADYOLKAVVYYG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 522 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
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TYPE: PRT ORGANISM: Pyrococcus furioeus

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141 SVSQIGADTVMHSLGYDGSGÝVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 200
                                                                                                                        201 GTHVAGIVAGTGSV*NSQYIGVAPGAKLVGVKVLGADGSGSVSFLIAGVDHVVQNKDKYG 259
                                                                                                                                         260 IRVINLSLGSSGSSDGTDSLEGAVNNAMDAGIVVCVAAGHSGPNTYTVGSPAAASKVITV 319
                                                                                                                                                                                                  320 GAVDSNDNIASFSSRGPTADGREKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTSM 379
                                                                                                                                                                                                                                                          380 ATPHYSGYGALILQAHPENTPOKYKTALIETADIYAPKEIADIAYGAGRYNVYKAIKYDD 439
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                                                                             500 YGFEKVGYYNPTAGTWTVK WSKKGAANYQVDVVSDGSLSQSGGGNPNPNPNPNPTPTD 559
                                                                                                                                                                                                                                                                                                                                                                                                                                            560 IQIPIGSVNDYWDTSDTFTP F/NSGATKITGDLTFDTSYNDLDLYLYDPNGNLVDRSTSS 619
                                             ς:
Ouery Match 62.24 Score 2138.5; DB 4; Length 522; Best Local Similarity 78.35; Pred. No. 1.40-144; Matches 407; Conservative 56; Mismatches 70; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 NSVEHVEYANPAPOTWIFFLY AVATYGMADYQLKAVVYYG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09435472; Patent No. 6358726; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TAKAKURA, HIKARU
APPLICANT: HORISHITA, MIO
APPLICANT: SHIMOJO, TOMOKO
APPLICANT: ASADA, KIYOZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-445-472-1
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US-09-445-472-4 'Sequence 4, Application US/09445472 'Patent No. 6358726 'GENERAL INFORMATION:

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Sequence 4, Application US/09000/16
Sequence 4, Application US/09000/16
Patent No. 614541
Patent No. 614541
CENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUDGLACK ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE TITLE OF INVENTION: ILE EXPERSSION PRODUCT
VUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AAGNSGPNIYTVGSPAAASKV TVGAVDSNDNIASESSRGPIADGRIKPEVVAPGVDIIA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 DGSGSVSTIIAGVDWVYQNKDKYGlKVINLSLGSSGSSDGTDSLSQAVNNAMDAGIVVCV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DGSGSVSTILAGVDWYVQDKDXXGIRVINLSLGSSQSSDGTDSLSQAVRNARDAGIVVCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 DLKGKVIGWYDAVNGRSTPYDIGGGGTINVAGIVAGTGSVNSOYIGVAPGAKLVGVKVLGA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14: Score 1148; DB 1; Length 237; Pred. No. 1.6e-74; Indels 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 PRASGISMGIPINDYYTKASGISMAIPHVSGVGALILGAHPSWIPDKVKT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
WEDIUM YPPE: DISKette: $.5 inch, 1.44 mb
WEDIUM TYPE: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: NS-108
                                                                                  PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-JUN-16:524
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1994,130236
FILING DATE: 13-JUN-1994,
PRIOR APPLICATION NUMBER: 1994,133912
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT NUMBER: 25-JUL-1994
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                        ALONEL/PROPER 25.616
REGISTRATION NUMBER: 25.616
REGISTRATION NUMBER: WITA-1
TELECOMUNICATION INFORMATION:
TELEFRONE: (202) 628-5197
TELEFRONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/03/753,532
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-1-03
SOFTWARE: Wordperfect 3:
CURRENT APPLICATION DATA.
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Best Local Similarity 97.0%;
Matches 223; Conservative
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amino acid
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STATE: D.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-000-016-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 SVSQIGADIVWNSLGYDGSGVVVAIVDIGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 YAKLIFIGSVADKGSATHIFDVSGATFVIATLYWDIGSSDIDLYLYDPNGNBYDYSYTAY 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 GAYDSNDNIASFSSRGPTADGRLKPEVYAPGYDIIAPRASGTSMGTPINDYTTKASGTSM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 GAVDKYDVIISPSSRGPIADGRLKPEVVAPGNWIIAARASGISMGQPINDYYTAAPGISH'247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 ATPHYSGUGALILOAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRYNVYKAIKYDD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 IRVINLSLGSSOSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 SAAQWATYWW.-LGYDGSGITTGIIDTGIDASHPDLQGKVIGWVDEWNGRSYPYDDHGH'67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
49.7%; Score 1707; DB 4; Length 412;
Best Local Similarity 80.6%; Pred; No. 5.3e-114;
Matches 325; Conservative 29; Mismatches 47; Indels 2
                         APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAXAKURA-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALCHIN VETSION 3.0
SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08750532
Sequence 18, Application US/08750532
Patent No. 5756339
GENERAL INFORMATION:
APPLICANT: MITTA, MAGAINTA, MILTA, MAGAINTA, MILTA, MAGAINTA, SUSUMUA APPLICANT: TSUNASAWA, SUSUMUA APPLICANT: KATO, IKUNOSHIN TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENE NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 YGFEKYGYYNPTAGTWTVKVVSYKGAANYQVDVVSDGSLSQSG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IMP PC COMPATIBLE
COMPOTER: IMP PC COMPATIBLE
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pyrococcus furiosus
US-09-445-472-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-750-532-18
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Sequence 2, Application US/0900016
Patent No. 643541
ENERAL INFORMATION: AAIGA ACTAIN APPLICANT: AAIGA ARISAGA & C. A. TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE NUMBER OF BEOLENEES: TOTAIN ACTAIN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGTHYAGIVAGIGSVN-SCHIGVARGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKOKY 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 LAAPVKEVVRNNAVQQKNYGLLEPGLERKVQRMNWNQEVDTVINEGSYGDRDRAVKVLRL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 EAGELRFTLTSLNADAVRSSHED: -- ASELWDAVTNGDRTASGIAHVWLDGVRRAALDTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.34; Score 665; DB 4; Length 823;
Best Local Similarity 31.24; Pred. No. 2.16-39;
Matches 216; Conservative 84; Mismatches 269; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REACABLE FORM:
HEDIUM TYPE: DISKette, 3:5 inch, 1.44 mb
COMPUTER: BM COMPACIBLE
OPERATING SYSTEM: MS-TOS
SOFTWARE: WOORDS-IDLE
OSFTWARE: WOORDS-IDLE
OSFTWARE: WOORDS-IDLE
OSFTWARE: WOORDS-IGCT, 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/00,016
FILING DATE:
ATTOR APPLICATION NUMBER:
FILING DATE:
ATTOR APPLICATION NUMBER:
FILING DATE:
ATTOR APPLICATION NUMBER: SERVENCE/COCKET WINBER:
ATTOR APPLICATION NUMBER: SERVENCE/COCKET WINBER: SERVENCE/COCKET WINBER: SERVENCE/COCKET WINBER: TELECOMMUNICATION INFORMATION:
                                -----AKPLSAT---IGYTYDTAG 733
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INFORMATION FOR SEQ ID NO: 23
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TELEPAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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; MOLECULE TYPE: protein
US-09-000-016-2
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                                                                                                            RESULT 11
US-09-000-016-2
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19.3%; Score 665; DB 4; Length 734; St. Best Local Similarity 31.2%; Pred. No. 1.8e-39;
Matches 216; Conservative 84; Mismatches 269; Indels 124; Gaps 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 VSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTP--YDDG3 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 HGTHVASIAAGTGAQSKGKKKGVAPGAAILNGKVLDDSGPGDDSGILAGMEMAAQ----;320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 LPADAARLVASGKLDRREFDITELG--KAATRNSSKOGLKVIV---GYGGAARAAKBUR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 MGAQYKYSYKIIPAVAVKIKARDLLLIAGHIDTGYFGNTRVSGIKFIQEDXKVQVDDATS:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 HGTHYAGIVAGTGSVN-SQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIRVINLSLGSSQSSDGTDSLSQAVNN-ANDAGIVVCVAAGNSGPNTYTVGSPAAASKVI;317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 TVGAVDSNDNIASFSSRCP-TADGRLKPEVVAPGVDIIAPRASGISMGTPIND---YYIK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 ALOCTVIADPVSVSFGVOCMPHTDDEPVTKOLTYRNLGTQDVTLKLTSTATDPKGKARPA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVVSY------KGAANYQVDVVSDGSLSQSGGGNPNPNPNPTPTTDTQTF--- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVESYDVTVRHIGRDGKPTTEHLTDLIGYAGLGSGRGYG------APATDTATLTLP 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 TGS-VNDYWDTSDTFTW-----NVNSGATKITGDLTFDT-SYNDLDLYLXDPNGMLV 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 LAAPVKPVVRNNAVQQKNYGLLIPGLFXKVQRMNWNGEVDTVINFGSYGDRDRAVKVLRL 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 ASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAFKEIADIAYGAGRVNVYK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIK----YDDYAKLTFFGSVADKGSAFH 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 TFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPIAGTWTV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555 GFFLGATTVTVPA---GGSASVDMTADTRLGGTVDGAYSAYVATGGGGTVRTAAAVQR 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRSTSSNSYEHVRYANPAPGIWIFLVYAYSTYG 646
APPLICATION NUMBER: US/09/000,016
FILING DATE: January 30, 1998
                   FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REERENCE/COCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 734 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-000-016-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 TVKVVSY------K3AANYQVDVVSDGSLSQSGGGNPNPNPNPNPTDTDTQTF- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 OREVESYDVTVRHIGRDCK?TTEHLTDLIGYAGLGSGRGYG------APATDTATLR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 YKAIK-----YDDYAKLIFTGSVADKGSA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 TKASGTSMATPHVSGVGALILGAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNV 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 KYGIRVINLSLGSSQSSDGTDSLSQAVNN-AWDAGIVVCVAAGNSGPNTYTVGSPAAASK 315
                                                                                                                                                                                                                                                                                                                                          316 VIIVGAVDSNDNIASFSSRGP-TADGRLKPEVVAPGVDIIAPRASGISMGTPIND---YY 371
                                                                                                                                                                                                                                                                                                                                                                                                                              140 TSVSQIGADTVWNSLGYDGSÅV KVA IVDTGIDANHPOLKGKVIGMYDAVNGRSTP--YDD 197
                                                                                                                                                                                                                  198 QGHCTHVAQIVAGTGSVN-SQYLQVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 THTEDVSGATEVTATLYMDYGESSIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAGTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 DKALOQTVIADPVSVSFQVQQMP=:DDDEPVTKQLTYRNLGTQDVTLKLTSTATDFKGKAA
                                                                                                                                                     Query Match
Best Local Similarity 35.9%; Pred. No. 2e-38;
Matches 179; Conservative 5%; Mismatches 177; Indels 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Shih, Jason C. H.
APPLICANT: Shih, Jason C. H.
APPLICANT: Miller, Eric S.
APPLICANT: Miller, Eric S.
APPLICANT: Miller, Eric S.
APPLICANT: Miller, Eric S.
TITLE OF INVENTION: DWD-A XERATINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Gibley
STREET: Post office Drawer 34009
CITY: Charlotte
STATE: NO 5712147th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IN PC COMPATIBLE
COMPUTER: IN PC COMPATIBLE
COMPUTER: IN PC COMPATIBLE
OPERATION SYSTEM: PC-1025/MS-DOS
SOFTWARE: PACEDIN RELEASE #1.0, Version #1.25
SOFTWARE: PACEDIN DATE:
CURRENT APPLICATION DATE:
FILLING DATE: 24-JUL 1896
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 250,028
PRIOR APPLICATION DATE: 2997
FILLING DATE: 27-MAY-3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/00685774 Patent No. 5712147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 LPKGTYLVDSWIAKDFGTL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 -- TGS-VNDYWDTSDTETM 579
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COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-685-774-2
US-09-000-016-7
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APPLICANT: ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-FIHYDROPYRIDINE DERIV
TITLE OF INVENTION: ITS EXPRESSION PRODUCT
TOTALE OF INVENTION: ITS EXPRESSION PRODUCT
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STREET: U.S.A.
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 TGS-VNDYWDFSDTFTM-----NVNSGATKITGDLTFDT-SXNDLDLXLXDPNGNLV 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          663 KGTYLVDSWIAKDEGTLKGGIDWLVQPKLSVTKDT-TLTLDARTTKAADITVPDPK---- 717
                                                                                                                                                                                                                                                                                                                                                                             518 KVVSY -----KGAANYQVDVVSDGSLSQSGGNPNPNPNPNPNPTTDTQTF--- 563
                                                                                                                                                                                                                                                                                                                                                                                                                      612 EVESYDVTVRHIGRDGRPTTEHLTDLIGYAGLGSGRGYG------APATDTAILRLP 662
                                                                                                                                                                                                                                       495 ALOQTVIADPVSVSFGVQQWPHTDDEPVTKQLTYRNLGTQDVTLKLTSTATDPKGKAAPA 554
                                                                                                                                                                                                                                                                                                                             555 GFFTLGATTVTVPA---GGSASVDMTADTRLGGTVDGAYSAYVVATGGGGTVRTAAAVQR 611
     318 TVGAVDSNDNIASPSSRGP-TADGRLKPEVVAPGVDIIAPRASGTSMGTPIND----YYTK 37$
                                                                                                374 ASGISMAIPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYK 433
                                                                                                                            434 AIK-----YDDYAKLTFTGSVADKGSATH 457
                                                                                                                                                                                                                                                                                  458 TFDVSGATFVTATLVNDTGSSDIDLYLYDPNGNEVDYSYTATYGFEKVGYINPTAGTWTV 517
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Mordperfect 5.1
CURRENT APPLICATION NUMBER: US/09/000,016
PILING DATE: January 30, 1998
CLASSIFICATION: 530
PRICHATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614 DRSTSSNSYEHVEYANPAPGTWTFLVYAYSTYG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09000016
Patent No. 6143541
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REDISTRATION NUMBER: 33,367
REPERNCE/POCKET UNBER:
TELECOMUNICATION
TELEPHONE: 202-711,8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 520 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-09-000-016-7
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ATTORNEY/AGENT INFORMATION:

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Sequence 1. Application US/08'41'395A
Patent No. 5811490
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RUDBS, John C.
TITLE OF INVENTION: Ascorbic Acid, 2'keto-L'Gulonic Acid, and Esters of TITLE OF INVENTION: 2'keto-L'Gulonic Acid, and Esters of NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
16.2%; Score 557.5; DB 1; Length 350;
Best Local Similarity 37.5%; Pred. No. 2.98-32;
Matches 146; Conservative 56; Mismatches 134; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 NQEVDTVIMEGSYGDRDRAVK VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGNIDT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AY------VEEDEVEHALAQTVPYGIPLIKADKV-QAQGFKGANVKVAVLDTGIQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GYFGNTRVSGIKFIQEDVKVQVEDAT---SVSQIGADTVHNSLGYDGSGVVVAIVDTGID 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 ANHPDLKGKVIGWYDAVNGRSTPYDDOGHGTHVAGIVACTGSVNSOYIGVAPCAKLVGVK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 VLGADGSGSVSTIIAGVD#MYQNKDKYGIRVINLSLGSSQSSDGTDSLSGAVNNAWDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 VYCVAAGNSGP--NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 GYDIIAPRASGISMGTPINDWWWYARSGISMATPHYSGYGALILQAHPSWTPUKVKTALIE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Region
LOCATION: 1.76
OTHER INFORMATION: /note* "The region from 1 to 76 is
31-JUL-2892
7N: 435
                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 TADIVAPKEIADIAYGAGRVINTRA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 TATYLG----SSFYYGKGLIN/EAA 348
                                TUPULOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-923-260A-4
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US-08-845-295A-1
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16.3%: Score 560.5; DB 1; Length 379;
Best Local Similarity 39.0%; Pred. No. 2e-32;
Matches 150; Conservative 53; Mismatches 133; Indexs 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                57 NOEVDTVIMFGSYGDRDRAVK--VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 G------AGVYSTYPTHTATT-LNGTSNVSPHVAGAAALILSKHPNLSASQVRNRLSS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 AY------VEEDHVAHALAQTVPYGIPLIKADKV-QAQGFKGANVKVAYLDTGIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 ANHPDLKGKYIGWYDAVHGRSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVK 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 GVDIIAPRASGTSMGTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTA%IE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 VLGADGSGSVSTIIAGVDHVVQNKPKYGIRVINLSLGSSQSSDGTDSLSQAVNNAHDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 GYFGNTRVSGIKFIQEDYKVQVDDAT---SVSQIGADTVHNSLGYDGSGVVVAIVDTGID [17]
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Gerard J. Weiser
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
       NAME: SIDLEY, KENDETH D.
REGISTRATION NUMBER: 31,665
REFERENCE/OCKET NUMBER: 5051-260
TELECOMMULICATION INFORMATION:
TELEPHONE: (919) 420-2200
TELEPAX: (919) 881-3175
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/07923260A
Petent No. 571901
Petent No. 571901
Petent Incommitted
APPLICANT: Incuye, Masayori
TITLE OF INVENTION: PROTEIN ACTIVATION
NUMBER OF SEQUENCES: 13
CORRESONDENCE ADDRESS:
                                                                                                                                                                                                                                        ORGANISM: Bacillus licheniformis
STRAIN: PWD-1
US-08-685-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 TADIVAPKEIADIAYGAGRVNVYKA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            LENGTH: 379 amino acids
                                                                                                                                                                       NOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19102
COMPUTER READABLE FORM:
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Ouery Match 16.2%; Score 557.5; DB 2; Length 379;
Best Local Similarity 37.3%; Pred. No. 3.3e-32; Indels 49; Gaps 13;
Hatches 146; Conservative 56; Mismatches 134; Indels 49; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 GVDIIAPRASGTSMGTPINDYYTKASGTSWATPHVSGVGALILQAHPSWTPDKVKTAN E 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 GAGUYSTYPTST-----YATLNGTSMASPHVAGAAALILSKHPNLSASGVRNRLSS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 ANHPDLKGKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVNSQY1GVAFGAKLVGVK 2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 VVCVAAGNSGP--NTTTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 AY-----VEEDHVAHALAQIVPYGIPLIKADKV-QAQGFKGANVKVAVLDIGIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 GYFGNTRVSGIKFIQEDYKVQVDDAT --- SVSQIGADTVMNSLGYDGSGVVVAIVDTGID 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 VLGADGSGSVSTIIAGVDWYVQNKDKYGIRVINLSLGSSOSSDGTDSLSQAVNNAWDAGI (29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 VLNSSGSGITSGIVSGIEWATTN----GMDVINNSLG---CPSGSTAMROAVDNAIANGY 25
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: 18M Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,295A
PILICA DATE: 25-APIL1-97
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/017.879
RICHENG ARE: 17-MAY-1996
ATTOR APPLICATION DATE: US 60/017.879
REDISATION NUMBER: US 60/017.879
REDISATION NUMBER: 38,346
REDISATION NUMBER: 38,346
REDISATION NUMBER: 38,346
REDISCOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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Kingsport
: Tennessee
RY: USA
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Search completed: October 31, 2002, 13:32:26 Job time : 17 secs

us-09-841-553-1.rpr

Page 1

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 31, 2002, 13:27:48 : Search time 17 Seconds (without alignments) 3724.875 Million cell updates/sec

US-09-841-553-1 3437 1 MKRLGAVVLALVLVGLLAGT......rayStygwadYolkavvyyg 659 Perfect score: Sequence:

283138 seqs, 96089334 residues Scoring table: BLOSUM62 . Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution.

SUMMARIES

100		Description	ij.	1	14			Subtilisin 30 3.4	-	42	microbial series n		alkaline proteinas	Subtilistr (F) 2 A	1 6	**	T TDD DISTABLE COLUMN	The property of the property o	Subcilisin (EC 3.4		Subtilisin (EC 3.4		Subtilisin (EC 3.4	high-alkaline seri	thermitase (BC 3.4	serine proteinase	Subtilisin.type pr		alkaline serine pr	aqualysin (EC 3, 4		subtilis; n.type a:	alkaline proteinas	
SOMMAKIES		a	A60407	00000	TABCOG	10000	139/80	· VSROS	STRAIL	SUBSD	A41341	JC1085	JC4802	8//0#0	SUBSI	A4977B	A36734	SUBSS	301487	423624	087	001001	10 A C C C C C C C C C C C C C C C C C C	CHAPTA	110001	10000	203/31	900700	204208	A35742	7,000	007.00	2027	
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Intradellular alkalina serina proteinase aprx - Bacillus subtilis

C; Date: 05-Dec-1997 sequenca_revision 05-Dec-1997 ftext_change 15-Oct-1999

C; Accession: A6587

R; Kunst, F; Ogasawara, N; Moser, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R; Erini, S.; Broullet, S.; Brischi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Nature 390, 249-256, 1997

R; Authors: Foulger, D.; Fries, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiczi, A; Habart, A.; Hibbert, M.; Holsappal, S.; Hosono, S.; Hullo, M. Aluthors: Lauber, D.; Fries, V.; Lee, S.; Kumano, M.; Kurita, R.; Lupidus, A.; Lardino, Y.; H.; Holsappal, S.; Hosono, S.; Hullo, M. Aluthors: Lauber, J.; Lazarevic, V.; Lee, S.; Kumano, M.; Kurita, R.; Lupidus, A.; Lardino, Y.; H.; Ogawa K.; Ogiwara, D.; Cazarevic, V.; Lee, S.; Kumano, W.; R.; Lub, H.; Masuda, S.; Mullo, Y.; M.; Rioger, M.; Rioder, G.; Pertrai, A.; Tenstein, G.; Rocche, B.; Rocche, B.; Rock, B.; Rose, M.; Sadale, X.; Scanlakeuth, M.; Tamakoshi, A.; Tenstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, T.; Schroeter, P.; Terpstra, P.; Tenstein, C.; Yoshikawa, H.; Danchin, A.; Reference number: A69580; MulD; 98044033

A; Residues: Preliminary; nucleum, acquence not shown; translation not shown
A; Residues: 1-442 (KUN)
A; Residues: 1-442 (KUN)
A; Crongarence of the Gram-postive bacterium Bacillus subtili

A/Cross-references: GB:299113: 유묘:AL009126; NID:92634090; PIDN:CAB13610.1; PID:e11833 A:Experimental source: strain 관용

A/Gene: aprx C/Superfamily: subtilisin home3.09y F/146-398/Domain: subtilisin hemology <SBT>

127 FIQEDYKVOVDDATSVSQIGARRIVANSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYD 186 Query Match
19.5% Score 669.5; DB 2; Length 442;
Best Local Similarity 46.01 Pred. No. 4.1e-29;
Natches 151; Conservative 51: Mismatches 103; Indels 23; Gaps ò

246 AGVDWVVQ-NKDK--YGIRVINLSLGSS---QSSDGTDSLSQAVNNANDAGIVVCVAAGN 299 8 ò

300 SGPNTYTVGSPAAASKVITVSKOSSN-----DNIASFSSRGPTADGRLKPEVVAPGVD 352 g ò

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subtilisin (EC 3.4.21.62) Sendul precursor - Bacillus sp.
C.Species: Bacillus sp.
C.Species: Bacillus sp.
C.Jaccession: 19-Jul-1996 #sequence, as tision 19-Jul-1996 #text_change 22-Jun-1999
C.Jaccession: 139780
R.Yamagata, V.; Isshiki, K.; (10) shima, E.
Brayme Histob. Trechnol. 17, 6+8,661, 1895
A.Fitle: Subtilisin Sendul from Alkalophilic Bacillus sp.: molecular and enzymatic pr.
A.Reference number: 139780; https://documer.iiii.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Reference.com/A.Refere
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A, Molecule Lype: Publishing associated with the onset of sporulation, and m C; Commont: Secretion of subtlikely is associated with the onset of sporulation, and m C; Commont: Secretion of subtlikely.
C; Commont: Secretion of subtlikely.
C; Commont: Secretion of subtlikely.
C; Superfamily: subtlikely subtlikely.
C; Superfamily: subtlikely protein, hydrolase; Serine proteinase
C; Superfamily: subtlikely sequence % fight of secretion of Sight 
A:Wolecule type: DNA
A;Residues: 1-379 <JAC
A;Residues: 1-379 <JAC
A;Residues: 1-379 <JAC
A;Residues: 1-379 <JAC
A;Cross-references: GB:X03341; NID:g487721; PIDN:CAB56500.1; PID:g5921206
A;Cross-references: GB:X03341; NID:g6816
B;Smith, E.L.; DeLange, R.J.; Ryans, W.H.; Landon, M.; Narkland, F.S.
J; Blol. Chem. 243, Jah4-2191, 1368
A;Title: Subtilisin Carlsberg, W. The complete sequence; comparison with subtilisin I
A;Reference number: A00968; MUID: 68234702
A;Accession: A00968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 VYCVAAGNSGP--NIYIVGSPAASKVITVGAVDSNDNIASFSSRGPTADGRLKPBVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 GVDIIAPRASGTSMGTFINDYYTNASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIE 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 NQEVDTVINEGSYGDRDRAVK+;VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDT 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.2%; Score 557.5; DB 1; Length 379; Best Local Similarity 37.9%; Pred. No. 3.88-23; Matches 146; Conservative 55; Mismatches 134; Indels 49.
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R; Jacobs, M; Elisason, M; Uhlen, M; Plock, J.I.

R; Jacobs, M; Elisason, M; Uhlen, M; Plock, J.I.

A; Fille: Cloning, sequencing and expression of subtiliain Carlaberg from Bacillus lichen A; Reference number: A24111; NUID:86093688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP001513; GB:BA000004; NID:q10174345; PIDN:BAB05649.1; GSPDB:GN00 B. Experimental Bource: strain C-125 C;Genetics: A;Gene: aprX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ritakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Euji, F.; Hira Nucleic Acids Res. 28, 4317-431, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus alodurans and A;Reference number: A83650; MuID:20512582; PMID:11058132
A;Reference number: A83650; MuID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intracellular alkaline serine proteinase aprX [imported] - Becillus halodurins (strain C;Species: Bacillus halodurens (c;Species: Bacillus halodurens (c;Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 15-Jun-2001;C;Accession: B83891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                            353 IIAPRASGT-----SNGTPINDYYTKASGTSMATPHYSGYGALILQAHPSWTPDKYKFAL-407
                                                                                                                                                             GTPINDYYTKASGISNATPHVSGVGALILQAHPSHTPDKVKTALIETADIVAPKELAD 3. 423
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; Pred. No. 2.3e-27;
68; Mismatches 122; Indels 36; Gaps
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Local Similarity 39.2%;
hes 146; Conservative 68
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427 YGAGYISAEGAI 438
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A; Molecule type: DNA
A; Residues: 1-444 <STO>
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In The Engymes, 3rd ed., vol.3, Boyer, P.D., ed., pp.547-560, Academic Press, New Yor A.Title: Subtilisin: X-ray structure.
A.Fible: Subtilisin: X-ray structure.
A.Contents: annotation: X-ray crystallography, 2.5 angstroms; active site not necessary for normal sportulation.
                                             A: Molecule type: protein
A: Residues: 108-162, 'PN', 165-167, 'D', 169-194, 'SA', 197-204, 'DA', 207-264, 'ST', 267-357, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrolysin (EC 3.4...) - Pyrococcus furiosus (5)Species: 15-Oct-1999 #sequence_cavision 15-Oct-1999 #text_change 24-Oct-2000 Rivorhorst, W.G.B.; Eggen, R.I.b.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vo A.Title: Isolation and charactarization of the hyperthermostable scrine procease, pyr A.Reference number: 220481; WGND:96353370
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A:Experimental source: DSM3638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 VERLMGAQVKYSYKIIPAV.∵;-...AVKIKARDLLLIAGMIDTGYFGNTRVSGTKFIQE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 DYKVQVDDAT----SVSQIGADŤVWNSLGYDGSGVYVAIVDTGIDANHPDLKGKVIGWYDA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 DHVAHAYAQSVPYGVSQIKAPAL-HSQCYTGSNVKVAVIDSGIDSSHPDL--KVAGGASN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 VPSETNPFQDNNSHGTHVAGTYAALNN-SIGVLGVAPSASLYAVKVLGABGSGQYSWIN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 GVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAMDAGIVVCVAAGNSGP--NT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 GIEWAIAN----NMDVINNSLG---GPSGSAALKAAVDKAVASGVVVVAAAGNEGTSGSS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 TLPGNKKGATNGTSMASP3VÄGAAALILSKHPNWTWTQVRSSLENTT----TKLGDSPY 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 YIVGSPAAASKVIIVGAVDSHDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMG 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VNCRSTPY-DDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                              A.Start codon: GTG
C.Superfamily: subtilisin; subtilisin homology
C.Reywords: hydrolase; sering proteinase
E.1-32/Domain: signal sequence; stackus predicted <SIG>
F.13-107/Domain: activation peptide istatus predicted <APT>
F.108-382/Product: subtilisin pPN' status experimental <AMT>
F.130-342/Domain: subtilisin homology <SBT>
F.139-171,328/Active site: ASR: Nis, Ser status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 15'34', Score 533.5', DB 1, Length Best Local Similarity 38.54; Pred. No. 7.79-22, Matches 143; Conservative 52; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: preliminary; translator; from GB/EMBL/DDBJ
A:Nolecule type: DNA
A:Residues: 1-1398 <VOO>
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C;Keywords: hydrolase; serine proteinase
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Nytlernéte names: subtilisin Novo
(Species: Bacillus amyioliquefaciens)
C.Species: Bacillus amyioliquefaciens
C.Species: 24-Apr-1984 Sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
C.Accession: B25415, A93463, A92033, A00970
J. Bacteriol. 159, 811-819, 1984
A.Fitle: Genes for alkaline processe and neutral protease from Bacillus amyloliquefacient A.Reference number: A.Sf415; MUID: 85006739
A.Recession: B25415
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Stations: 1.382 **C485**
Residues: 1.382 **C485**
Residues: 1.382 **C485**
Residues: 1.382 **C485**
Residues: 1.384 **C485**
Reference: ATCC 23844
Feneral source: A
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R:Markland, F.S.; Smith, E.L.
A: Blol. Chem. 242, 5198-5211, 1967
A:Tile: Subtilisin BPN'. VII. Isolation of cyanogen bromide peptides and the complete A:Reference number: A92033; MUID:68086682
                                                                                                                                                                                        16 / Gaps 17,
                            58 QEVD----TVIMFGSYGDRDRAVKVLRLMGAQVKKSYKIIPAVAVKIKARDLLLIAGÄID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 IGYFGHTRVSGIKFIQEDYKVQYDDATS---VSQIGADTVWNSLGYDGSGVVVAIVDTGI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 -----EKDPSITYIEEDIEVTITNOVIPWGITRVOAPIAM-IRGYIGIGVRVAVLDIGE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 DANHPOLKGKVIGWYDAVNGRSTPYDDQGHGTHYAGIVAGTGSYNSQYIGVAPGAKLVGV 2%0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 KVLGADGSGSVSTIIAGVDWVVQNKDKKGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAG 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 KVLGANGSGSVSSIAQGLQWTAQN----NIHVANLSLGSPV---GSQTLELAVNOATNAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 IVVCVAAGHSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 VDIIAPRASGTSMGTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIET 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSDKGQSEMSLFAEVNDESIEMELL-------95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 VLVVAATGNNGSG--TVSYPARYANALAVGATDONNNRASFSQYGTGLN-----IVAPG 309
                                                                                                                                                                                                                                                      1 MKRLGAVVL---ALVLVGLLAGTALAAPVKPVVRNNAVOOKNYGLLTPGLFKKVQPHHHH 57
                                                                                                                                                                                                                                                                                                       Length 382;
                                                                                                      Query Match
15.9%; Score 547; DB 2; Length 382;
Best Local Similarity 34.5%; Pred, No. 1.4e-22;
Matches 134; Conservative 73; Mismatches 145; Indels
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MAICULD type: DNA
Residues: 'W', 8-382 <WE2>
C;Keywords: hydrolase; serine proteinase F;136-342/Domain: subtilisin homology <SBT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ATSLGNSN----OFGSGLVNAEAATR 382
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Length 1398;

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Indels 467; 'Gaps (2) 37;
                                                                                                                                              120 EKAWLNREVKLSP-PIVEKDVKTK-EPSLEPKMYNSTWVINALOFIQEFGTDGSGVVVAN 378.00.
                                                                                                     60 MKGOPMNYLIIKTKEGKLEEAKTELEKLGABILDENRVLNMLLVKIKPEKVKELNYISSL.119.00
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                                                                                                                                IDTGYFGNTRVSGIKFIQEDYKVQVDDATSVSQIGADIVWNSL-----GYDGSGVVVAI (165)
                                                                                                                                                                                               827 HDYG-----LYRPDGMEVFPYQLDYLPAA------VSNPMPGNWELVWTGFNPAPL 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           872 YE-----SGFLVRIHGVEITPS------VWYINRTYLDTNTEFSIEFNITNI, 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 ------ADXGSATHT-FDVSGATFVT-----ATLY (472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767 DPTTPVIEDEILNTIVIPEKFTPENNYTLIWYDINGPENVTHHFFTVPEGVDVLYAMTTY 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 WDTGSSDIDLYLYDPNG-----NEVDYSYTAYYGFEKVGYKNPTAGTWIVKVVSYKCAAN 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707 IKXVGDTEYRTPELYATEPWIKPFVSGSVILENNTEPVLRVKYDVEGLEPGLYVGRXLID 3766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTSMATPHVSGVVALLISGPRPEGIYYNPDIIKKVLESGATWLEGDPYTGGKYTELDÖG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAKLVGYKVLGADGSGBVSTIIAGVDWVVQNKDKYGIRVINLSL-GSSQSSDCTDSLSQA 782
                                                                                                                                                                                                                                                                                                                                                                                              -----SNDNIASPSSRGPTADGRLKPEVVAPGVDIIAPRASGTSWGTPINDYYTKA 374
                                                                                                                                                                                                                                                     238 TLNESTGLMEYVVKTVYVSNVTIGNITSANGIYHFGLLPERYFDLNFDGDQEDFYPVLL7 297.
                                                                                                                                                                                                                                                                                                                           194 -PYDDQCHGTHYAGIYAGIYAGISVN-----SQYI--------GVAP 322
                                                                                                                                                                                                                                                                                                                                              2 KRLGAVVLALVLVGLLAGTALAAPVKPVVRNNAVQQ--KNYGLLTPGLFKKVQRMMN-- 57
                                                                                                                                                                             VDTGIDANH-----PDLKGKVIGWYD------190
                                                                                                                                                                                                                                                                                                 298 NSTGNGYDIAYVDTDLDYDFTDEVPLGQYNVTYDVAVFSYYXGFLNYVLAEIDPNGEXAV 357
                                                                         58 ---QEVDTVIMEGSYGDRDRAVKVLRLMGAQVKYSYKIIPAVAVKI---KARDLLLIAGM 111
                                                   4 KGLTVLFIAIMLLSVVPVHFVSAGTPPVSSENSTTSILPNOQVVT----KEVSQAALNAI 59
                                                                                                                                                                                                                                  606 YDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLVYAYS 643
Best Local Similarity 22.6%; Pred, No. 4.3e-21;
Matches 239; Conservative 104; Mismatches 248;
                                                                                                                                                                                                                                                                                        191 RST-----
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microbial serine proteinase (%C 0.4.21.-), minor (vpr), precursor - Bacillus subtilis Sipacies acillus subtilis Subtilis
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Bill. Chem. Hopper-Seyler 368, 147-1487, 1987
Bill. Chem. Hopper-Seyler 368, 147-1487, 1987
Bill. Chem. Hopper-Seyler 368, 147-1487, 187-1487
Bill. Chem. Hopper-Seyler 368, 147-1487
A. Accession: 302492
A. A. Accession: 302492
A. A. Accession of subtilisin is associated with the onset of sportlation, and more necessary for normal sportlation homology
C. Superfamily: subtilisin is subtilisin homology
C. Superfamily: subtilisin protein, hydrolase, serine proteinase
C. Superfamily: subtilisin protein, hydrolase, serine proteinase
F. 32-244/Domain: subtilisin homology ASBT>
F. 32-224/Domain: subtilisin homology ASBT>
F. 32-224/Domain: subtilisin homology ASBT>
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                                                                                                                                                                                     subtilisin (EC 3.4.21.62) DY - Eaclilus subtills (strain DY)
subtilistin (EC 3.4.21.62) DY - Eaclilus subtills (strain DY)
NALecrade names: alkaline serine proteinage
C;Species: Bacillus subtilis
A;Variety: strain DY
A;Variety: strain DY
C;Date: 20-sep-1384 *Sequence_revision 20-sep-1384 *text_change 02-Jul-1998
C;Date: 20-sep-1384 *Sequence_revision 20-sep-1384 *text_change 02-Jul-1998
C;Accession: A00965;S02492
C;Accession: A00965;S02492
Biol: Cfam. Hoppe-Seyter 366, 121;A30, 1985
Biol: Cfam. Hoppe-Seyter 366, 121;A30, 1985
Biol: Cfam. Hoppe-Seyter 366, 121;A30, 1985
Biol: Cham. Hoppe-Seyter 366, 121;A30, 1985
Biol: An A;Accession: A00969; MuiD;85279896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 -NTYTVGSPAAASKVITVGAKTSUDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 IIAGVDWVVONKDKYGIRVINLSLGSSQSSDGTDSLSOAVNNAMDAGIVVCVAAGNSGP- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNGTPINDXYTKASGTSMATEHVSGVGALILOAHPSWTPDKVKTALJETADIVAPKEIAD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GIKFIQEDYKVQVDDATSVSQEGADTVWNSLGYDGSGVVVAIVDIGIDANHPDLKGKVIG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.38; Score 524.5; DB 1, Length 274; 42.28; Pred. No. 1.5e-21; t.tve. 38; Mismatches 94; Indels 49.
973 YDSKGNLVALDGNPTAEEEVVVEYPKPGVYSIVVHGYS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAYGAGRVNYKA 434
|| | | | | | |
FYYGKGLINVEAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US.3%:
Best Local Similarity 42.2%:
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 1-274 <NED>
                                                                                                                                                             RESULT 7
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A: Molecule type: DNA	Db 375 KALNNKEVELVEAGIGEANDEBGKDLTGKVAVVKRGSIAFVDKADNAKKAGAIGMVVYNN 434
ArkeBlouds: 1-806 KELO> Arcross-references: GB:N76590; NID:gl43819; PIDN:AAA22881.1; PID:g143820 A.Accoss(on: A4141	Oy 3281ASFSSRGP 336
A Woldcule type: protein	Db 435 LSGEIEANVPGMSVPTIKLSLEDGEKLVSALKAGETKTTFKLTVSKALGEQVADFSSRGP 494
Richaser. P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, A. Pannort G. Dannhin A.	OY 337 TAD-GRLKPEVVAPGVDIXAPRASGISMGTPINDY-YTKASGISMATPHVSGVGALLLOA 394
MOL. Narpoport, 50, 20minuta, 50. MOL. Microbiol. 10, 371-384, 50. Mol. Mol. Mol. Mol. Mol. Mol. Mol. Mol.	Db 495
A/Reference number: S39655, WID:9502057.	Oy 395 HPSWTPDKVKTALIETADIVAPKEIADIAYGAGNVNVKAIKYDDYAKLTFTGSV 449
A.Residues: 1-806 ccia> A.Cross-references: EMBL:X73124; NID:q413923; PIDN:CAA51601.1; PID:q580871	OV 450 ADKGSATHTEDVSGATEV-ATLYMDTGSSDIDLYLYDDNGNEVDYSYTAYYGFEKVGYYN
R:Kunst, F.: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azèvedo, V.; Berter C.; Baron, S.; Broullet, S.; Bruschi, C.Y.; Caldvell, B.; Capunso, V.; Carter, N.M.; Ch A. Fhritch, C. D. Francisco, D.T.: Entita	DD 600VSPGSYSYGTELKENNETETIENGSSIRKSYTLEYSENGSGI
Nature 390, 249-256, 1997 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.: Galizzi, A.; Galler	OY 510 PTACTWTVKVVSYK-GANNYQVDVVSDGSLSQSGGGNPNPNPNPNPNPNPTPTTDTQTFTGSV-
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosonoj S.; Hullo, N.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	Db 647 STSGTSRVVIPAHOTGKÄTÄKVKVNTKKTKAGTVEGTVI
A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, R.; Masuda, S.; Maueell y, N.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl'jajiM.; Portetelld Rieger, M.; Rivolla, C.; Rocha, B.; Roche, B.; Rose, M.; Sadate, V.; Satò, P.; Scanlon,	Oy 568SYNDLDLY 604 O
A. Authors: Schleich, S., Schroeter, R.; Scoffone, F.; Sekguchi, J.; Sekowska, A.; Serod akeuchi, M.; Tanaka, T.; Terpstra, P.; Toononi, A.; Toosato, V.; Uchiyama,	OV 605 LYDPNGNLYDRSPSSMSYEHVEYANPAPGTWTFLVYA 641
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.A.Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, N. A.A.	Db 741 VYDSNLDFAGQAGIYKNÇÜKGYÖYEDWDGTINGGTKLPA-GEYYLLAYA
A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A:Reference number: A69580; MUID:98044033	
A:Accession: D69730 A:Status: preliminary; nucleic acid sequence not shown; translation not shown	RESULT 9 JC1085
A; Molecule type: DNA A; Residues: 1-806 < KUN>	subtilisin (EC 3.4.21.62) precugor · Bacillus licheniformis N:Alternate names: alkaline proteinase
A;Cross-references: GB:299123; GB:AL009126; NID:g2636240; PIDN:CAB15625.1; PID:g2636344 A;Experimental source: strain 168	C; Species: Bacillus lichenishemis C; Date: 09-Aug-1995 #sequenca_revision 19-Oct-1995 #text_change 31-Mar-1997
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of d C:Genetics:	C: Accession: JC1085 R:Lei, H.; Hong, Y.; Zhang, Z.?. Shen, T.J.
A:Gene: vpr A:Start codon: TTG :Superfamily: mirrohial serine protestnase upr: subtilisin homology	Chinese Blochem. J. 9, 441-467 1993 A 7.Title: PCR analitying, ctp3ing and sequencing of the coding sequence of the beforeing number. To 7085
C: Keywords: hydrolase; serine proteinse F: 1-28/Yoman; signal sequence status predicted <sig></sig>	A. Accession: 301085 A. Molecule type: DNA
F:180.548/Domain: propertue status predicted <f:180.548 *status="" <sbt="" atypical="" domain:="" homology="" subtilisin=""></f:180.548>	Alloce: The translation of the start codon ATG is not given in this paper A. O. C. D. C.
Query 'Natch 15.2%; Score 522.5; DB 2; Length 806; Best Local Similarity 24.7%; Pred. No. 8.1e-21; Matches 190; Conservative 102; Mismatches 208; Indels 269; Gaps 30;	C. Reyecrds: hydrolase; series grottain sometopy C. Keyecrds: hydrolase; series grottainase F:24-235/Domain: subtilisin hydrology <sbt> F:33, 64,221/Active site: Asp. His, Ser #status predicted</sbt>
QY 72 RDRAVKVLRLMGAQVKYSY-KIIPAVAVKIKARDLLLIAGMIDTGYFGUTRV 122 ::: : : : : : : :	Query Match 15.1%; Score 519.5; DB 2; Length 275; Best Local Similarity 42.3%; Pred. No. 2.8e-21; Matches 132; Conservative: 38; Mismatches 94; Indels 49; Gaps
Qy 123 SGIKFIQEDYKVQVDDATSVSQIGADTVWNSLGYDGSGVVVALVDTGIDANHPDLKG 179 : : :	QY 124 GIKFIQEDYKVQVDDATSVSQIGADTVANSLGYDGSGVVVAIVDTGIDANHFDLKGKVIG 183
QY 180 KVIGWYDAVNGRSTPYDDQCHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGV 230 : :	QY 184 WYDAVNGRSTPYDDQGHGSAVAGIVAGTGSVHSQYIGVAPGAKLVGVKVLGADGSGSVST 243
QY 231 KVLGADGSGSVSTIIAGVDWYVONKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAVDAG-290° 1 1 1 1 1 1 1 1 1 1	QY 244 IIAGVDWVVQNKDKYGIEVÎNLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGP-302
Oy 291 IVVCVAGUSCPNTYTVGSPAAASKVITVGA	OY 303 -HTYTVGSPAAASKVINVGAVINSNDNIASESSRGPTADGRLKPEVVAPGVDIIAPRASGT 361
	SWGTPINDYYTKASGTSWATPSWSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIAD

sequence of the alkalin

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A; Residues: 107-381 <5U2>
A; Residues: 107-381 <5U2>
A; Residues: 107-381 <5U2>
A; Residues: 107-381 <5U2>
A; Rechart, M.; Nomura, K.; Hcng, K.; Ito, Y.; Asada, A.; Nishimuro, S.
Blochem. Blophys. Res. Communa, 187, 1340-1347, 1993
A; Title: Purification and characterization of a strong fibrinolytic enzyme (nattokina A; Reference number: JC2036; MJDD: 34107337
A; Accession: JC2036
                                                                                                                                                                                                                                                                                                                                                                                                                                  aprN, of Bacillus subtilis (
subtilisin (EC 3.4.21.62) NAT precursor - Bacillus subtilis (strain natto NC2-1) NiAlternate names natto proteinase, nattokinase; subtilis BSP C;Species: Bacillus subtilis: sub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AAASKVITVGAVDSNDNIASFESRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDY 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 PYDD-QGHGTHVAGIVAGIGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVV 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross-references: GB:D25319; NID:g435439; PIDN:BAA04989.1; PID:g435440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keyvords: hydrolase, serine proteinase; zymogen
1-29/Domain: signal sequence #status predicted <SIG>
30-106/Domain: activation postide #status predicted <PRO>
1107-381/Product: subtilisit with #status experimental <MAT>
1129-441/Domain: subtilisit formology <SBT>
1139,170,327/Active site: Asp, Ser, His, Ser #status predicted
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Best Local Similarity > 36.3%, Pred. No. 9.2e-21;
Matches 139; Conservative < 52; Mismatches 124; Indels 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ragaku To Seibutsu 29, 119-123, 1991

Kagaku To Seibutsu 29, 119-123, 1991

A) Title: Natto kinase and fibrinolysis.

A) Reference number: JS0601

A) Accession: JS0601

A) Accession: JS0601

A) Reference number: JSSUA

R; Suni, H: Nakajina, N.

Nippon Nogeikagaku Kaishi 65, 115-1127, 1991

A) Title: Studies on fibrinolysis anzymes in fermention food.

A) Reference number: JS0517

A) Accession: JS0517
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Start codon: GTG
Superfamily: subtilisin; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: protein
Residues: 107-381 <FUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: JH0778
A, Molecule type: DNA
A, Residues: 1-381 <NAK>
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C; Superfamily: subtilisin, subtilisin homology
C; Superfamily: subtilisin; serine proteinase
F; 1-25, Domain: signal sequence **status predicted <SIG>F; 1-25, Domain: signal sequence **status predicted <PRO>F; 106, Domain: propeptide **status predicted <PRO>F; 107-383/Product: alkaline proteinase **status experimental <WAT>F; 144, Domain: subtilisin homology <SBI>F; 143, 176, 330/Active site: Asp, His, Ser **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alkaline proteinase (EC 3.4.21.-) precursor - Thermoactinomyces sp. (strain E79) Cispectes: Thormoactinomyces sp. (strain E79 A.Variety: strain E79 E.A.Variety: strain E79 & Sequence_revision 15-oct-1996 *text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JC4802
A; Molecule type: DNA
A; Residues: 1-384 <LEE>
A; Residues: 1-384 <LEE>
A; Crossures: references: GB:U31759; NID:g1389689; PIDN:AAB36499.1; PID:g1683629-
A; Experimental source: strain E79
C; Comment: This protein is thermostable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 EVDTVIMEGSYGDRDRAVKVLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 NTRVSGIKFIQEDYKVQV----DDATS----VSQIGADTVWNSLGYDGSGVVVAIVDTGI. 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 DANHPDEKGKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGV (213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 KVLGADGSGSVSTIIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAC, 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 RVLNINSGSGIMAAVANGIAYAAQN----GADVISLSLG---GISGSSALQSAVQAWNSG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 IVYCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 AVVVAAAGNS--SSSIPNYPAYYSQAIAVASIDSNDSLSYFSNYGSWVD-----VAAPG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDIIAPRASGISMGIPINDYYIKASGISMAIPHVSGVGALILQAHPSWIPDKVKTALIE® 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKRLGAVVLALVLVGLLA--GTALAAPVKPVVRNNAVQQKNYGLLTPGLFKKVQRMNWN 58
                                            206 YSTYPTNTYAT-LNGTSMASEHVAGAAALILSKHPNLSASQVRNRLSSTATYLG----SS
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ADKISG---TGTYFQHGRINAYKAVNY 384
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                                                                                                                                                                                                                                    | | | :|| |
261 FYYGKGLINVEAA 273
                                                                                                                                                                    422 IAYGAGRVNVYKA 434
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A;Nap position: 690-771
A;Start codon: GTG
C;Function:
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us-09-841-553-1.rpr
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                                                                                                                                                                                                                                                                                                                                                                                          Subtilisin (EC 3.4.21.62) E precursor - Bacillus subtilis

N.Alternate names: sikaline proteinase; bacillopeptidase E; extracel: liar alkaline serin

C; Secties: Bacillus subtilis

C; Secties: Bacillus subtilis

C; Accession: A00972, A5616; I39970; I39779; 568012; H69586

R; Stahl, M.L.; Ferrari, E

J. Bacteriol. 158, 411-418, 1984

A; Title: Replacement of the Bacillus subtilis subtilisin structural generation in vitral A; Reference number: A00972; MUD: 84212198

A; Molecule type: DNA

A; Residues: 1-381 <57A->
A; Molecule type: DNA

A; Residues: 1-381 <57A->
A; Molecule in a serial in 168

R; Wong, S:L.; Price, C.W.; Goldfarb, D.S.; Doi, R.H.

R; Wong, S:L.; Price, C.W.; Goldfarb, D.S.; Doi, R.H.

A; Title: The subtilisin E gene of Bacillus subtilis is transcribed from a sigma37 promot

A; Archerence number: A0216; MUD: 84144862
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A. Rolecule type: DNA

A. Bruilch, S.D. Gasawara, N. Berter

A.; Ehrlich, S.D. Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabrat, C. Ferrari, E. Nature 390, 249-256, 1997

A. Rollech, D. Fritz, C.; Fulita, M.; Fullech, Y.; Fuma, S.; Galizzi, A.; Galler tech, J.; Rarwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hospiel, A.; Lardinois, S.; Maueel, M.; Kurite, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lardinois, A.; Lardinois, A.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.W.; Portetelld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
facilutes: 1-155 cmon>
Cross-references: 0.8K01443; NID:9143665; PIDN:AAA22814.1; PID:9143666.
IKemura, H.; Takagi, H.; Inouyo, N.
1. Blol. Chem. 262, 7859-7864, 1987
Title: Requirement of pro-sequence for the production of active subtillisin E in Escher
Reference number: 139969; MuID:87222417
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A:Molecule type: DNA
A:Roalduga: 1-156 CIKE>
A:Roalduga: 1-156 CIKE>
A:Cross-references: GB.M16639, NID:9143521, PIDN:AAA22744.1; PID:9143523
B:Hemner, D.J.; Perradi, E.; Perego, M.; Hoch, J.A.
A:Bacteriol, 170, 296-300, 1988
A:Title: Location of the targets of the hpr-97, sacU32(Hy), and sacO36(Hy) mutations in A:Accession: 139778; NUID:88086885
A:Accession: 139778
A:Accession: 139778
A:Accession: DAA, Crossinated from GB/EMBL/DDBJ
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.71tte: Bacillus subtilis subtilisin gene (aprE) is expressed from a sigma-A (sigma-43).
Reference number: 139779, WUID:89213955
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A: Residues: 1-13 <PAR>
A: Ramal, W.: Hoeceg. J.O.: Kales. R.: Shafqat, J.: Razzaki, T.: Zaida. 1.3: Joernvall, R: Ramal, W.: 1304, 363-366, 1995
A: Title: Isolation. characterization and structure of subtilisin from a thatmostable Bac A: Accession: 568012; WUID: 96069945
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Residues: 1-8 <HEN>
Cross-references: GB:M19125; NID:9142527; PIDN:AAA22245.1; PID:9342528
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                                                                                                                                                                                                                  431 VYKA 434
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Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadalo, Y.; Sato, T.; Scanlakathuris: Schlelch, S.; Schroeter, R.; Scoffene, F.; Sekiguchl, J.; Sakowaka, A.; Sakouchi, M.; Tamakoshi, A.; Tanakoshi, A.; Tanakothi, A.; Tanak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A pescription: catalyzes the hydrolyss of peptide bonds
A Pathway: protein digestion
A Pathway: protein digestion
A Pathway: protein digestion
A Pathway: protein digestion
C Superfamily: subtilisin; subtilisin homology
C Superfamily: subtilisin; subtilisin homology
C Superfamily: subtilisin; subtilisin protein homology
C Superfamily: subtilisin; subtilisin predicted <SIG>
E:1.23/Domain: styling sequence fistatus predicted <ART>
E:24.106/Domain: activation peptide satatus predicted <ART>
E:107-381/Product: subtilisin B satatus predicted <ART>
E:129-341/Domain: subtilisin homology <SDT>
E:138.170,327/Active site: ARE, HIS, Ser fistatus predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 YAOSYPYGISOIKAPAR, HSGG:TGSNVKVAVIDSGIDSSHPDL--NVRGGASFVPSETN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 PYDD-QGHGTHVAGIVAGT/35V4SQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVV 252
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14.9%: Score 512.5; DB 1; Longth 381;
Best Local Similarity 37.9%: Pred. No. 1e-20;
Matches 138; Conservative: 53; Mismatches 124; Indels 49
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A/Residues: 1-1433 <KUN>
A/Ross-references: GB:299111: Cu:299112; GB:AL009126; NID:92633902; PIDN:CAB13404.1;
A/Experimental source: strain CE3
                                                                                                                                                                      A, Molecule type: DNA
A, Residues: 1.380 cVAN>
A, Residues: 1.380 cVAN>
A, Residues: 1.380 cVAN>
A, Residues: 1.380 cVAN>
A, Coss.references: GB.M65086; NID:9142456; PIDN:AAA22212.1; PID:9142457
A, Experimental source: strain PB92, ATCC 31408
A, Note: amino end of mature protein confirmed by peptide sequencing
B, Note: amino end of mature protein confirmed by peptide sequencing
B, Note: amino end of mature protein confirmed by peptide sequencing
B, Nosci. B, Nobayashi, T.; Kobayashi, M.; Yanamoto, M.; Nakamura, E.; Anono, R.; Horikc
B, Nosci. B, Notechnol. B, Nochem. 55, 1450, 1992
A, TILLE: Wolecular cloning, nucleotide sequence, and expression of the structural gene f
A, Reference number: JC1244, MUID:93043753
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multiple chromosomal integration of a pacillus
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A Accession: JC1244
A Accession: JC1244
A Modela type: DNA
A Mosiques: 1-195, 72, 197-380 <TAK>
A MOSIQUES: 1-195, 72, 197-380 <TAK>
A COOST TEEPERON OF SELUTION NOT A MOSIQUES: 1-195, 72, 195, 721)
A COOST TEEPERON OF SELUTION SUBSTITUTION NOT A MOSIQUE CONTROL OF SELUTION OF SELUTION NOT A MOSIQUES: 2 MOSIQUES CONTROL OF SELUTION 
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14.9%; Score 510.5; DB 2; Length 380;
Best Local Similarity 32.9%; Pred. No. 1.3e-20;
Matches 146; Conservative 75; Mismatches 148; Indels 75;
                           A;Title: Cloning, characterization, and mu
A;Reference number: A49778; MUD:91282483
A;Accession: A49778
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A Molecule type: DNA
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A Residues: 1410-1433 AMS>
A Cross-references: EMBL:X17344; NID:940165; PIDN:CAA35224.1; PID:9809661
A Cross-references: EMBL:X17344; NID:940165; PIDN:CAA35224.1; PID:9809661
A Kato, T.; Vamagata, Y.; Aral. T.; Inhishima, E.
Biosci, Blockenhol, Blocken. 56, 1166-1168, 1992
A; Title: Purification of a new extracellular 90-kDa serine proteinase with isoelectric A, Reference number; JN0335; MUD:93005071
A; Accession: JN0335
A; Molecule type: protein
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A; Residues: 876-935, 'CG' <WU2>
A; Cross-references: 68-105400; WID: 9119197
A; Cross-reference has been corrected
A; Mother: this sequence has been corrected
A; A; Accession: S08223; MU; 30174995
A; Accession: S08223
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A;Notecute rype in anterial was Bacillus subtilis (natto)
A;Note: source of this anterial was Bacillus subtilis (natto)
A;Note: source of this anterial was Bacillus subtilis (natto)
A;Note: source of this anterial was Bacillus subtilis homologs of Escherichia of A;Title: Cloning and character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and character.ization of A;Title: Cloning and character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of A;Title: Cloning and Character.ization of Bacillus subtilis homologs of Escherichia of Character.ization of Bacillus and Character.i
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A;Molecule type: DNA
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 KLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYG-----IRVINLSLGSSGSSDGTDS 278
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                                                                                                                                                                                                                                                                            RLISSVLSTVYISSLLFPGAAGASSKVTSPSVKELQSAESIONKISSSLKKS-FKKKEK 66
                                                                                                                                                                                                                                                                                                                  54 MNWNGEVDTVIMFGSYGDRDRAVKVL-----RLMGAQVKYSYKIIPAVAVKIKA----102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVIG------WYDAVNGRSTPYDDQGHGTHVAGIVAGIGSVNSQYIGVAPGA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSQAVNNAWDAG-IVVCVAAGNS-----GPNTYTVGSPAAASKVITVGAVDSNDNIASF 331
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                                                                                                                                                                     Query Match
14.8%; Score 510; DB 1; Length 1433;
Best Local Similarity 26.4%; Pred. No. 8.3e-20;
Matches 210; Conservative 104; Mismatches 302; Indels 178; Gaps
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                                                                                                                                                                                                                                           3 RLGAVVLALVLVGLL----AGTALAAPVKPVVRN-----NAVQOKNYGLLTPGLFKKVQR 33
A Map postLich 135 (degrees)
C; Superfamily: bacillopeptidase F; subtilisin homology
C; Superfamily: bacillopeptidase F; subtilisin homology
C; Seywords: extracellular protein; hydrolase; serine proteinase
F; 1-30/Domain: signal sequence fatatus predicted csig>
F; 11-144/Domain: superide fatatus predicted csig>
F; 115-143/Protouct: bacillopeptidase F stratus experimental cMAT>
F; 118-466/Domain: subtilisin homology cspr
F; 127, 274, 452/Active Bite: Asp, His, Ser fstatus predicted
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subtilisin (EC 3.4.21.62) amyiosacchariticus precursor - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: 24-Apr-1984 sequence_ravision 24-Feb-1995 #taxt_change 16-Jun-2000
C;Accession: 444448; A00971; 655013
R;Yoshimoto, T: Oyama, H:Forda, T: Tone, H: Takeshita, T:; Kamiyama, T:; Tsuru, J: Biochem: 103, 1060-1065, 1908
A;Title: Cloning and expression of subtilisin amylosacchariticus gene.
A;Reference number: A41448; K!ID:89008194
A;Accession: A41448
A;Accession: A41448
A;Residues: 1-381 </vo>
A;Cross references: GB:D00264; NID:9216328; PIDN:BAA00186.1; PID:9912425
A;Experimental source: var. amylosacchariticus
R;Kurihara, M: Markland, F:S: Smith, E.L.
J: Biol. Chem: A77, 5619-5631, 1972
A;Reference number: A00971; M:JID:72266688
A;Accession: A00971
A;Ancession: A00971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: protein
A:Residues: 107:112-114;148-152;155-157;164-170;173-174;178-181;200-205;210-212;219-2
A:Residues: 107:112-114;148-152;155-157;164-170;173-174;178-181;200-205;210-212;219-2
B:Xesidues: 107:112-114;148-152;155-157;164-170;173-174;178-181;200-205;210-212;219-2
B:Xesidue: 107:112-114;148-152;155-157;164-170;173-174;178-181;200-205;210-212;219-2
FEBS Lett. 374, 363-366, 1995
FEBS Lett. 374, 363-366, 199
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A;Nolecule type: protein
A;Residues: 107-235,77-345,293-381 <KAM>
C;Comment: Secretion of subtilisin is associated with the onset of sporulation, and minct necessary for normal sporulation.
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C.Keywords: extracellular procein; hydrolase; serine proteinase
F:107-381/Product: subtilisfs. #stratus predicted cMAT>
F:129-341/Domain: subtilisin homology cSBT>
F:128.170,327/Active site: Asp, His, Ser #status predicted
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Search completed: October 31, 2002, 13:31:55 Job time : 23 secs

OM protein - protein search, using sw model

October 31, 2002, 13:25:28 ; Search time 10 Second* (without alignments) 2551.618 Million cell updr::sr/sec Run on:

US-09-841-553-1 3437 1 MKRLGAVVLALVLVGLLAGT......YAYSTYGWADYQLKAVVYYG 639.

Title: Perfect score: Sequence:

105224 seqs, 38719550 residues Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/ennounce/or send an email to license@isb-sib.ch).
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PRINTS: PR00723; SUBTILISEA:
PROSITE: PS00136; SUBTILISEA:
PROSITE: PS00137; SUBTILASE_HIS: 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
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                                                                                                                                        K02496; AAB05345.1; -.
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259
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1502: 15-JAN-92.
158H: 07-DEC-95.
158L: 07-DEC-95.
158N: 31-JAN-94.
                                                                                                                                                            PIR A00970; SUR PDB: 1500 PDB: 1501 15-00 PDB: 1501 14-00 PDB: 1701 11-00 PDB:
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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MISCELLANEOUS: SECRETION OF SUBTILISIN IS ASSOCIATED WITH ONSET OF SPORULATION, AND MANY MUTATIONS WHICH BACK SPORULATION, ANT EARLY STACES AFFECT EXPRESSION LEVELS OF SUBTILISIN. HOWEVER, STRILLISIN IS NOT NECESSARY FOR NORMAL SPORULATION.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genes for alkaline protease and neutral protease from Bacillus myloliquefacters contain a large open reading frame between the regions coding for signal sequence and mature protein."
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 108-382,
MEDLINE-68086682; PubMed-6065094;
MEDLINE-68086682; PubMed-6065094;
MEDLINE-68086682; PubMed-6065094;
"Subtline BPN: VII. Isolation of cyanogen bromide peptides and the complete amino acid sequence."

J. Blol. Chem. 242:5198-5211(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
Gallagher T., Oliver J., Bott R., Betzel C., Gilliland G.L.,
'Subtlistin BPN' at 1.6-A resolution: analysis for discrete disorder
and comparison of crystal forms.'
Acta Crystallogr. D 52:1125-1135(1956).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR. MEDLINE-85033707; Pubmed-6387152; Altaul Y.; Iltaka Y.; S., Akagawa H., Mitsul Y.; Iltaka Y.; "Grystal structure at 2.6-A resolution of the complex of subtilized BPN' with streptomyces subtilish inhibitor."; J. Mol. B101. 178:389-413(1984).
                                                                                                                                                                                                                                            MEDLINE-84069812; PubNed-6316278; Wells J.A., Chen E.Y.; Wells J.A., Perrail E., Henner D.J., Estell D.A., Chen E.Y.; "Cloning, sequencing, and secretion of Bacillus amyloliquefaciens subtilisin in Bacillus subtilis."; Nucleic Acids Res. 11:7911-7925(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-72035041; Pubmed-4399039;
Alden R.A., Wright C.S., Kraut J.,
"A hydrogen-bond network at the active site of subtilisin BPN'.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:119-124(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large increases in general stability for subtilisin BPN' through incremental changes in the free energy of unfolding.";
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MEDLINE-90057412; PubMed-2684274;
Pantollano M.W., Whitlow M., Wood J.F., Dodd S.W., Hardman K.D.,
Rollence M.L., Bryan P.N.;
          STRAIN-ATCC 23844;
MEDLINE-85006739; Pubmed-6090391;
Vasantha N., Thompson L.D., Rhodes C., Banner C., Nagle J.,
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Adrolase; Sporulation; Serine protesse; Zymogen; Signal; SUBTILISIN BPN'
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63; Gaps 14;
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                                                                                                                                                                                         DB 1; Length 382;
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                         Score 533.5; DB 1;
Pred. No. 3.1e-23;
52; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
Pyrolysin precursor (EC 3.4.21..)
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STRAIN-VOl / DMS 3638;
MEDLINE-96355370; PubMed-8702780;
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38.5%;
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Matches 143; Conservative
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370 YGKGLINVQAA 380
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                                                                                                                                                                                                                                                                                         Voorhorst W.G.B., Eggen R.K.L., Geerling A.C.M., Platteeuw C., Siezen R.J., de Vos W.M.; Isolation and characterization of the hyperthermostable serine protease, pyrolysin, and its gene from the hyperthermophilic archaeon pyrocecus furiosus.;
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pfam; PROMOR2; Peptidase_88.

primy: PROMOR2; PEPTIDASE_88.

PROSITE; PROMOR3; SUBTILIARY ASP: 1.

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RI CATALYIOS SUBTILIST NO MATRACELLULAR ALKALINE SERINE PROTEASE,

C. I PUNCTION: SUBTILIST NO FATARACELLULAR ALKALINE SERINE PROTEASE,

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C. I CATALYIC ACTIVITY MYICIASIS OF PROTEINS AND PEPTIDE AMIDES.

C. I CATALYIC ACTIVITY SECRETCH OF SUBTILISIN IS ASSOCIATED WITH ONSET OF SORULATION, AND MANY MONATONS WHICH BLOCK SPORULATION AT EARLY

C. SUBCELLULAR LOCATION: Secreted.

C. SUBTILASE FAMILY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBJELIASE FAMILY:

C. SUBTILASE FAMILY.

C. SUBTILASE FAMILY:

C. SUBTILASE FAMILY:

SERVICE SUBSES.

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C. TALLONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE TALLONGS TO PEPTIDASE FAMILY.

C. TALLONGS TO PERTINE SECONDS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SECONDS TO PERTINANCE TO PERTINANCE SECONDS TO PERTINANCE TO 
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                                                                               913 YAPINATLIPIGEGTYNASYESVEDERFIKGIEVPEGTAELKIRIGNPSVPNSDLDLYL 972.
Query Match
Best Local Similarity 42.2%; Pred. No. 6.6e-23;
Matches 132; Conservative 38; Mismatches 94; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interproj 19800209; Peptidase_88.
Prints: PR00082: Peptidase_88.
PRINTS: PR007136; SUBTILIST.
PROSTE: P800136; SUBTILIST.
PROSTE: P800137; SUBTILIST.
PROSTE: P800137; SUBTILIST.
PROSTE: P800138; SUBTILIST.
PROSTE: P800137; SUBTILIST.
PROSTE: P800136; SUB
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Bacillus Incheniformis ...
Bacillus/Clostridium group;
Bacillus/Staphylococcus group;
Bacillus/Staphylococcus group;
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                   606 YDPNGNLVDRSTSSNSYEHVETANPAPGTWTFLVYAYS 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Subtilisin DY (EC 3.4.21.62).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AA
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                                                                                            Glaser P., Kunst F. Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer F., Freedan E., Santana M., Schneider E., Schweizer J., Vertes A., Bapoport G., Danchin A.; Bapoport G., Danchin A.; Bachilus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees."; Hol. Microbiol. 10:371-384(1993).

1- FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.

1- SUBCELLULAR LOCATION: Secreted.

1- FIM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTEOLYSIS.

SUBTILASE FAMILY: SULVINGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                    GASTVSGESYNTDGNGHGTHVAGTVAALDNTG-VLGVAPNVSLYAIKVLNSSGSGTYSA 105
                                                                                                                                  303 -NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASS1 361
          84 WYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVST 243
                                                                           IIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGP- 302
                                                                                                                                                          SMGTPINDXYTKASGTSNATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIAD 221
                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 161-195.
MEDLINE-92041574; PubMed-1938892;
Sloma A., Rufo G.A. Jr., Theriault K.A., Dwyer M., Wilson S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of the gene for an additional extracellular serine protease of Bacillus subtilis."; J. Bacteriol. 173:6889-6895(1991).
                                                                                                                                                                                                                                                                                                                                                                                                        01-DBC-1992 (Rel. 24, Created)
01-DBC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Minor extracellular protease VPR precursor (EC 3.4.21.-).
VPR OR IPA-45R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Bacillus/Clostridium group,
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                             806 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-168;
MEDLINE-95020537; Pubmed-7934828;
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                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                  422 IAYGAGRVNVYKA 434
                                                                                                                                                                                                                                                                                     Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI_TaxID=1423;
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P29141;
                                                                              244
                                                                                                            901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 VMDTWMIKPDISAPGVNI (*** STIPTHDPDHPYGYGSKQGTSWASPHIAGAVAVIKQA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 HPSWTPDKVKTALIETADIWAFKEIADIAY-----GAGRVNVYKAIKYDDYAKLTFTGSV 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 RDRAVKVLRLMGAQVKYSY-KIIPAVAVKIKARDLLLIAGMID------TGYFGNTRV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 KVIGWYDAVNG----RSTPY-D----OGHGTHVAGIVAGTGSVNSOYIGVAPGAKLVGV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 OYKG-YDFVDNDYDDXETPTGDPRGEATDHGTHVAGTVAANGTIK----GVAPDATLLAY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 KVLCADGSGSVSTIIAGYDEVYQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 KALNNKBVELVEAGIGEAKDFESKDLTGKVAVVKRGSIAFVDKADNAKKAGAIGMVVYNN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 LSGEIEANVPGMSVPTIKLSLÆDGEKLVSALKAGETKTTFKLTVSKALGEQVADFSSRGP 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 TAD-GRIKPEVVAPGVDIIAPRASGTSMGTPINDY-YTKASGTSMATPHVSGVGALILQA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....NQNSQA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 PIAGTWIVKVVSYK-GAANY@?DVVSDGSLSQSGGGNPNPNPNPTPITDIQIFIGSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGIKFIQEDYKYQVDDATSVS2IGADIVWNSLGYDGSGVVVAIVDTGIDANHPDLK---G
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( BY SIMILARITY).
( BY SIMILARITY).
( BY SIMILARITY).
                           InterPro IFR000209; Peptidase_S8.

Pfam: PF00225; PA: 1.

Pram: PF00225; PA: 1.

PROSTIE: PS00136; SUBTIL:3IN.

PROSTIE: PS00136; SUBTILASE_ASP; 1.

PROSTIE: PS00138; SUBTILASE_ASP; 1.

PROSTIE: PS00138; SUBTILASE_SER; 1.

Hydrolase; Serine proteasef "ymogen; Signal; Complete proteome. 21 28 FGNL 1.

PROPEP 29 160
                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 522.5; DB 1; Length 806; tharity 24.7%; Pred. No. 3.3e-22; Conservative 102; Mismatches 208; Indels 269;
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CHARGE RELAY SYSTEM (B
CHARGE RELAY SYSTEM (B
CHARGE RELAY SYSTEM (B
InterPro; IPR003137; PA.
InterPro; IPR000209; Pepticase_S8
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806 AA;
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Matches 190; Conserv
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ACT_SITE
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SEQUENCE
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us-09-841-553-1.rsp

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Nakamura T., Yamagata Y., Ichishima E.;

Nuclecoide sequence of the subtilisin NAT gene, aprn, of Bacillus a buttils (natto).;

Blosci. Biotechnol. Blochem. 56:1869-1871(1992).

IT CATALYZES THE HYDROLYSIS OF PROTEINS AND PEPTIDE ANIDES.

IT CATALYZES THE HYDROLYSIS OF PROTEINS AND PEPTIDE ANIDES.

IT CATALYZES THE HYDROLYSIS of PROTEINS AND PEPTIDE ANIDES.

IT CATALYZES THE HYDROLYSIS of PROTEINS WITH broad specification of peptide bonds, and a preference for a large uncharged residual in Pl. Hydrolyses peptide anides.

SUBCELLULAR LOCATION: SECRETION OF SUBTILISIN IS ASSOCIATED WITH ONSET OF SPORULATION, AND MANY MUTATIONS WHICH BLOCK SPORULATION AT SARLY STAGES AFFECT EXPRESSION LEVELS OF SUBTILISIN. HOWEVER, SUBTILISIN STACES AFFECT EXPRESSION LEVELS OF SUBTILISIN. HOWEVER, SUBTILIZIN C. SIMILARITY: BELONGS TO PEPTIDASE PANILY SB: ALSO KNOWN AS THE SUBTILISE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial contities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenselisb-sib.ch).
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SUBTILISIN NAT.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
DAED4816ED18A092 CRC64;
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Pfan: PP00082; Peptidase_S8.
PRINTS: PR00723; SUBTILISIN.
PROSITE: PS00136; SUBTILASE_ASP; 1.
PROSITE: PS00136; SUBTILASE_ASP; 1.
PROSITE: PS00138; SUBTILASE_ASP; 1.
Nydrolese; Spoulation; Serine protease; Zymogen; Signal.
PR0PEP 24 106 POTENTIAL.
                                                                                                                                                        Bacillus subtilis var. natto.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Stophylococcus group; Bacillus.
NCBI_TaxID-86029;
                                                                                                                  update)
                                         381 AA
                                                                   01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Subillisin NAT precursor (EC 3.4.21.62).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 513.5;
                                                                                                                                                                                                                                                               STRAIN-NC2-1;
MEDLINE-93113095; Pubmed-1369081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D25319; BAA04989.1; -: EMBL; S51909; AAC60424.1; -: PIR; J40778; J40778; HSSP; P07518; IMEE.
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 38.21
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
138
170
170
327
381 AA;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                   SUBN_BACNA
P35835;
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RESULT 6
SUBN_BACNA
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TATALLOGIAND (2.6 ANGSTRONS).

STAIN—168:

A BAIL THE 9903046; PUDNEd-9811547;

A BAIL THE 99030466; PUDNEd-9811547;

A BAIL S.C., Shinde U. L. Y., Indoye M., Berman H.M.;

A BAIL S.C., Shinde U. L. Y., Indoye M., Berman H.M.;

A BAIL S.C., Shinde U. L. Y., Indoye M., Berman H.M.;

A BAIL S.C., Shinde U. L. Y., Indoye M., Berman H.M.;

E-properiode complex at 12.0-% resolution.";

A MOL. BAIL SIGNIES THE WINDOLFSIS OF PROTEINS AND PEPTIDE ANIDES.

I CATALLYIC ACTIVITY: HYGICH'S OF PROTEINS AND EPTIDE ANIDES.

I CATALLYIC ACTIVITY: HYGICH'S OF PROTEINS AND EPTIDE ANIDES.

I PHYDIOLISE THE WINDOLFSIS OF PROTEINS AND AND EPTIDE ANIDES.

I PHYDIOLISE THE WINDOLFSIS OF STAIL BLOKE SPORULATION AT BAILY

C SPORULATION AND MANY HYMATIONS WHICH BLOKE SPORULATION AT BAILY

C STACES AFPECT EXPRESSER: EXPLES OF SUBPILIESIN HOWEVER, SUBTILISIN STAILS STAIL SEALS ALSO KNOWN AS THE STAIL STAIL SEALS.
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PYDD-OGHGTHVAGIVAGTGSVWSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVV 252
                                                                                                                           371 YTKASGTSMATPHVSGVGRLILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVN 430
                                                                                                                                                                                                                                                                                                274
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                                                                                                                                                                                                          253 ONKDKYGIRVINLSLG:50SSNGTDSLSQAVNNAWDAGIVVCVAAGNSGP--NTYTVGSP
                                                                                                                                                                                                                                                          222 SN----NHDVINNSLG---GPT:35TALKTVVDKAVSSGIVVAAAAGNEGSSGSTSTVGYP
                                                                                                                                                                                                                                                                                                                                   AAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDY
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168;
WEDLINE-84212198; PubMed-6427178;
SCBLIM.L., Ferrari E.;
"Replacement of the Bacilius subtills subtillsin structural on in vitro-derived deletion mutation.";
Bacteriol. 158:411-418(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacil.ms/Clostridium group,
Bacillus/Staphylococcus group; Bacillus.
NOBI_TaxID-1423,
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20-MAR-1987 (Rel. 04, Lect sequence update)
16-0cr-2001 (Rel. 40, Lest annotation update)
Subtilisin E precursor (Rt. 4, 4, 21, 62).
APRE OR APR OR SPAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 VQAA 379
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P04189;
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SUBT_BACSU
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38.2%; Pred. No. 4.2e-22; Lve 52; Mismatches 124; Indels 49; Saps

Watches 139;

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58 VISEKGGKVQKQEKTVNAAAATLDEKAVKEL-----KKDPSVAYVEEDH-IAHE 3.05--138 DATSV----SQIGADTVWNSLGYDGSGVVVALVDTGIDANHPDLKGKVIGWYDAVNGRST (9)

78 VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFGNTRVSGIKFIQEDYKVQV3 137

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-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
                                          X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS)
                                                                   MEDLINE-92390330; PubMed-1518788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M65086; AAA22212.1;
EMBL; A13738; CAA01128.1;
                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 112-380.
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Best Local Similarity 23.9%
Matches 145; Conservativa
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PDB; 1AH2; 15-APR-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; 508.001;
                                                               STRAIN-PB92
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SEQUENCE
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                                                                                                                                                                                                                                                                                                           Gaps. 13;
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MEDLINE-91282483; PubMed-2059048;
Van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hock R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 YTKASGTSMATPHVSGVGALILOAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVN 430
                                                                                                                                                                                                                                                                                                                                   78 VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFGNTRVSGIKFIQEDYKVQVD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 QNKDKYGIRVINLSIGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGP--NTYTVGSP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 AAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 AKYPSTIAVGAVNSSNORASFSSAGSELD-----VWAPGVSIQSTLPGGT----- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 PYDD-GGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVV 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 PYQDGSSHGTHVAGTIAALNN-SIGVLGVSPSASLYAVKVLDSTGSGOYSWIINGIBWAL 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 SN----NNDVINNSLG---GPIGSTALKIVVDKAVSSGIVVAAAAGNEGSSGSTSTVGYP 274.
                                                                                                                                                                                                                                                                                                                                                                                   138 DATSV----SQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRS: 193
                                                                                                                                                                                                                                                                               14.9%; Score 512.5; DB 1; Length 381;
1]arity 37.9%; Pred. No. 4.7e-22;
Conservative 53; Mismatches 124; Indels 49;
                                                                      MEACUS: SOCIOUS apre.
Subtiliate, BG10190; apre.
Interpro; IRR000209; Peptidase_S8.
Pfam; PF000023; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00136; SUBTILASE_BIS; 1.
PROSITE; PS00138; SUBTILASE_BIS; 1.
Hydrolase; Sporulation; Serine protease; Zymogen; Signal; ab-structure; Complete protease; DOTENTIAL.
12. POTENTIAL.
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SUBTILISTA E.
CHARGE RELAS SYSTEM.
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CHARGE RELAS SYSTEM.
47, 52269PGC22284824F CRC64;
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fol.AUG-1992 (Rel. 23, Lest sequence update)
T 15-UUL-1998 (Rel. 36, Lest annotation update)
T Alkaline protease precursor (EC 3.4.21.-).
Bacilius alcalophilus.
Bacilius/staphylococcus group; Bacillus/traklococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 380 AA.
                                                                                                                                                                                                                                                               39495 MW;
                       EMBL; X01988; AAA22742.1;
                                       IR; A00972; SUBSI.
DB; 1SCJ; 13-JAN-99.
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                                                                                                                                                                                                                                                                   381 AA;
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Matches 138; Conserv
                                                              MEROPS; S08.001;
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SEQUENCE
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ELYA_BACAO
ELYAO
ELYAO
AC P27693
DT 01-AUG
DT 01-AUG
DT 15-JUL
OS Bactel
OC Bactel
OC Bactel
OC Bactel
RN (1)
RN (1)
RN (1)
RN (2)
RX MEDLIN
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Sobok H., Hechl H.-J., Abhle'W., Schomburg D.;
Sobok H., Hechl H.-J., Abhle'W., Schomburg D.;
"X-ray structure determication and comparison of two crystal forms of a wrinant (Asnilsarg) of the wikeline protease from Bacillus alcalophilus refined at 7.85-% resolution.";
J. Mol. Biol. 228:108-117.1992). Martin J.R., Mudder F.A. Rarimi-Nejad Y., van der Zwan J., Martin J.R., Mudder F.A. Rarimi-Nejad Y., van der Zwan J., Mariani M., Schipper D., Boelens R.; Frotesse PB92 from Bacillus The solution structure of serine protesse PB92 from Bacillus alcalophilus presents a rigid fold with a flexible substrate-binding site."; ; "Cloning, characterization, and multiple chromosomal integration of Bacillus alkaline protesse gene."; Appl. Environ. Microbiol. 57:901-909(1991). Structure 5:521-532(1997).
Structure 5:521-532(1997).
-i. SUBCELBULAR LOCATION: Secreted.
-i. SIMILARITY: BELONGS TG PEPTIDASE FAMILY S8; ALSO KNOWN AS THE wan der Laen J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset C. Mulleners L.J.M., Dijstra B.W.;
Crystal structure of the high-alkaline serine protease PB92 from Bacillus alcalophilus.";
Protein Eng. 5:405-411(1992) DB 1; Length 380; Signal; 3D-structure. 143 CHARGE RELAY SYSTEM.
143 CHARGE RELAY SYSTEM.
125 CHARGE RELAY SYSTEM.
126 CHARGE RELAY SYSTEM.
1885,3 MM.: 539EA72771B6682C CRC64; 6.16-22; 14 9%; Score 510.5; 32 9%; Pred. No. 6.16 MEMORS, DOG. 701, 1 Interpro, 1 PROGOGOS, Peptidase_S8.

PEAM, PROGOGS, Peptidase_S8, 1.

PRINTS, PROGOTS, SUBTILASIA.

PROSITE, PSOGOTS, SUBTILASE_ASP, 1.

PROSITE, PSOGOTS, SUBTILASE_ASP, 1.

PROSITE, PSOGOTS, SUBTILASE_SER, 1.

PROSITE, PSOGOTS, SUBTILASE_SER, 1.

PATOLASS, Serine protease, Zymogen, Signa STGNAL.

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                                                                                                                                                                                                              258 VVAASGNSGAG--SISYPARYANAMAVGATDONNNRASFSOYGAGLD-----IVAPGVN 309
                                                                                                                                                                                                                                                      353 IIAPRASGISMGTPINDYYTKASGISMATPHVSGVGALILQAHPSWTPOKVKTALIETAD 412
                                                                                                                                                                                                                                                                       310 VOSTYPGST-----YASLNGTSNATPHVAGAAALVKOKNPSHSNVQIRNHLKNTAT 360
                               97 -----PAISYIEEDAEVITHAQSVPWGISRVQAPAAHNR-GLIGSGVKVAVLDIGI-S 147
                                                                                                                                                 116 YFGNTRVSGIKFIQEDYKVQVDDAT --- SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDA 1778
                                                                     173 NHPDLKCKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKV*2332
                                                                                       233 LGADGSGSYSTIIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIY 292
                                                                                                                                                                                            293 VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weinheim (1991).
-- SUBCELDULAR ELOCATION: Secreted.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning, nucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic Bacillus sp. 221.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-221 / ATCC 21522 / JCM 9139 / DSM 2512;
MEDLINE-93041753; Pubhed-1368952;
Takamil H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura ;
Aono R., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
(In) Horikoshi K. (eds.);
Microorganisms in alkaline evironments, pp.187-194, VCH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBL_taxID-79880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cillus sp. 221.";
.osci. Biotechnol. Biochem. 56:1455-1460(1992),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 112-129,
STRAIN-221 / ATCC 21522 / JCM 9139 / DSM 2512;
                                                                                                                                                                                                                                                                                                                                                                                                                       ELYA_BACCS STANDARD; PRT; 380 Aa. P41362; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Alkaline protease precursor (EC 3.4.21.*).
                                                                                                                                                                                                                                                                                                                                  361 SLGSTNL----YGSGLYNAEAATR 380
                                                                                                                                                                                                                                                                                                                  413 IVAPKEIADIAYGAGRVNVYKAIK 436
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01-FEB-1996 (Rel. 33, Latt sequence update)
01-FEB-1996 (Rel. 40, Last annotation update)
Bacillopeptidase F precursor (EC 3.4.21.-) (Estersse) (RP-I protesse)
BPR OR BPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 WNQEVDTVIMFGSYGDRDRAVKVLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 YEGNTRVSGIKFIQEDXXVQVDDAT---SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDA 172
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MEDLINE-90170864; PubMeG÷Ş106512;
Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
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173 173 CHARGE RELAX SYSTEM (BY SIMILARITY)
326 A326 CHARGE RELAX SYSTEM (BY SIMILARITY)
380 AA; 38826 MW; 5F73ABC68D5B6831 CRC64.
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14.2%; Score 510.5; DB 1; Length 380;
Best Local Similarity 32.5%; Pred. No. 6.1e-22;
Matches 146; Conservative 75; Mismatches 148; Indels 75;
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Bacillus/Staphylococcus group; Bacillus.
NCBI_TexID-1423;
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InterPro; IPR000209; Peptidase_S6.
Pfam: PR00022; Peptidase_S3: 1.
PRNTS: PR00723; SUBTILIASIN.
PROSITE: PS00136; SUBTILIASIN.
PROSITE; PS00137; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_SER; 1.
PROSITE; PS00138; SUBTILIASE_SER; 1.
PROSITE: PS00138; SUBTILIASE_SER; 1.
PROSITE: PS00138; SUBTILIASE_SER; 1.
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                                                     X.A.,
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                                                                                                    SEQUENCE FROM N.A.
MEDLINE-90216713; PubMed-2108961;
Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.;
Wu X.-Conjug, genetic organization, and characterization of a structural
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                                                                                                                                                                                                                                                                                                                                                                          Mesuda E.S., Anaguchi H., Sato T., Takeuchi M., Robayashi Y.; "Nucleotide sequence of the sporulation gene spoilGA from Bacillus subtilis.";
                                                          Sullivan B.J., Theriault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microria (1970)

Subtilist: 8610233; bpr.

InterPro; IPR00229; Peptidase_S8.

InterPro; IPR00229; Peptidase_S8.

PROWER: PRO0723; SUBTILISIN.

PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.

PROSITE; PS00136; SUBTILASE_SER; 1.

Hydrolase; Serine protease; Zymogen; Signal; Complete proteome.

SIGNAL

1 30 POTENTIAL.

PROPEP 31 194 POTENTIAL.

PROPEP 755 BACILLOPEPTIDASE F.

PROPEP 756 1433 POTENTIAL.
                                                                                                                                                                       Occupance of 1-211 FROM N.A. September 2139638, Beall B., Lowe M., Lutkenhaus J.; Beall B., Lowe M., Lutkenhaus J.; E.Coning and characterization of Bacillus subtilis homologs of Escherichia coli cell division genes fisz and fish."; J. Bacteriol. 170:4855-4864(1988).
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Sloma A., Rufo G.A. Jr., Rudolph C.F.,
                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 18:657-657(1990).
                                                                    Pero J.;
J. Bacteriol, 172:5520-5521(1990),
                                                                                                                                                                                                                                                                              STRAIN-168 / MARBURG;
MEDLINE-90174995; Pubmed-2106671;
Bacteriol, 172:1470-1477(1990)
                                                                                                                                                                                                                                                        [5]
SEQUENCE OF 1410-1433 FROM N.A.
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PIR, A35750; A35750.
PIR, A36734, A36734.
HSSP; P00782; SSBT.
MEROPS; SOB.017; -.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
T -> A (IN REF. 6).
A -> V (IN REF. 3).
KHONKA -> N (IN REF. 3).
OPOVLP -> RETLYS (IN REF. 3).
AOVSVVETG -> FCRSHKSV (IN REF. 3).
MISSING (IN REF. 3).
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NEDLINE-7226688 Pubmed-5055784;

NAUTHER M., Markhand F.S., Smith E.L.;
**Subtilisin Amylosacchariticus. 3 isolation and sequence of the "Subtilisin Amylosacchariticus." 1 isolation and sequence.";

"Subtilisin Amylosacchariticus. 3 isolation and sequence.";

"Subtilisin Paylosacchariticus. 3 isolation and sequence.";

"Subtilisin San Extraction San Extracti
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                                                                                                                                                                                              MEDIINE-72266687; PubMed-4560201;
Markland F.S., Kurihara M., Smith E.L.;
Subtilisin Amylosacchariticus, II. Isolation and sequence of the tryptic and cyanogen bromide peptides.";
J. Biol. Chem. 247:5602-5618(1972).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

**REDLINE=89008194; Pubmed=3139650;

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Kamiyama T., Tsuru D.;

**Cloning and expression of subtilisin amylosacchariticus gene.";

J. Blochem. 103:1060-1065(1988).
                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Subtilisin amylosacchariticus precursor (EC 3.4.21.62).
                                                                                                                                                                                                          Bacillus subtilis var. amylosacchariticus.
Bacterie: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
ACBI_TaxID-1483;
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                                                                       (Rel. 01, Created)
                    STANDARD;
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                                                                                               01-DEC-1992
15-DEC-1998
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SEQUENCE FROM N.A.

STALIN-BIOLOGY / KCTC-1823;

KA PEDLINE-9221938; PubMed-2.50743;

KA DELINE-9221938; PubMed-2.50743;

Adng J.S., Kang D.O., Chua M.J., Byun S.M.;

Jang J.S., Kang D.O., Chua M.J., Byun S.M.;

"Molecular cloning of subtilisin J gene from Bacillus

Rearchemophilus and K.E. expression in Bacillus subtilis.";

Blochem. Biophys. Res. Chran. 184.277-282(1952).

IT CATALIZES THE RUNCLYSIS OF PROTEINS AND PERTIDE ANDERS.

IT CATALIZES THE RUNCLYSIS OF PROTEINS AND PERTIDE ANDERS.

IT CATALIZES THE RUNCLYSIS OF PROTEINS AND PERTIDE ANDERS.

IT CATALIZES THE RUNCLYSIS OF SUBTILISIN MICH DROAD SPECIFICATOR OF SUBTILISIN IS ASSOCIATED WITH ONSET OF SPORULATION AND MARK. GUATATONS WHICH BLOCK SPORULATION AT EARLY

STAGES AFPECT EXPRENSION LEVELS OF SUBTILISIN. HOWEVER, SUBTILISIN

IS NOT NECESSARY FOR PURMAL SPORULATION.

IS NOT NECESSARY FOR PURMAL SPORULATION.
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                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 SN----NHDVINHSLC---GPSCSTALKTVVDKAVSSCIVVAAAAGNEGSSGSSGTVGYP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 AAASKVITVGAVDSNDNIESESSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDY 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 YTKASGISMATPHVSGVGALLAQAHPSWTPDKVKTALIETADIVAPKEIADIAVGAGRVN 430
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                                                                                                                                                                                                                                                                                                                                                                                                                               58 VISEKGGKVQKQFKYVNA.AATLDEKAVKEL-----KKDPSVAYVEEDH-IAHE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 DATSV----SQIGADTVWWSLCYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRST 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 PYDD-QCHGTHVAGIVAG@GSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDHVV 252
                                                                                                                                                                                                                                                                                                                                                                                    78 VLRLMGAQVKYSYKIIF VAVKIKARDLLLIAGMIDTGYFGNTRVSGIKFIQEDYKVQVD 137
                                                                                                                                                                                                                                                                                                                              Gapa
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                                                                                                                                                                                                                                                   14.8%; Score 509.5; DB 1; Length 381; 37.5%; Pred. No. 7e-22; tive 54; Mismatches 124; Indels 49;
365 7 M -> D (IN REF. 2)... 251BADE22B4824F CRC64;
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Bacillus/Staphylococcua group; Geobacillus.
NCBI_TaxID=1422;
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01-DEC-1992 (Rel. 24, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Subillistn J precursor (EC 3.4.21.62).
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                                                                                                                                                                                                                                                                                       Best Local Similarity 37.58
Matches 137; Conservative
                                                                                                                                                                    381 AA;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/&nnounce/or send an email to license@isb-sib.ch).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.8%; Score 509.5; DB 1; Length 381; 37.6%; Pred. No. 7e-22; 1ve 54; Mismatches 124; Indels 49;
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01-APR-1988 (Rel. 07, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Subtilisin (EC 3.4.21.62) (Alkaline mesentericopeptidase).
                                                                                                                                                                   PROBLET OF 19800209; Peptidase_S8.

PRAM: PF00082; Peptidase_S8; 1.

PRINTS; PR00723; SUBTILISIN.

PROSITE; PS00136; SUBTILASE_ASP; 1.

PROSITE; PS00137; SUBTILASE_HIS; 1.

PROSITE; PS00138; SUBTILASE_HIS; 1.

PROSITE; PS00138; SUBTILASE_RIS; 1.

PROSITE; PS001081; SUBTILASE_RIS; 1.

PROSITE; PS001081; SUBTILASE_SIS; 1.

POTENTIAL.

1 99 POTENTIAL.
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1408;
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Svendsen I., Genov N., Idakieva K.,
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                                                                                          EMBL; M64743; AAA22247.1;
PIR; JO1487; JO1487.
HSSP; P04189; 1SCJ.
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381
138
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Matches 137; Conserv
                                                                                                                                                       S08.001;
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REPARTMENT CRYSTALLOGRAPHY (2.7) ANGSTROMS).

RA HEDLINE-92172311; PubMed-A.V.7.3542;

RA HEDLINE-92172311; PubMed-A.V.7.3542;

RA DAUGET Z., Betzel C., Gencer N., Pipon N., Wilson K.S.;

Complex between the subt. 1.sin from a mesophilic bacterium and the series between the subt. 1.sin from a mesophilic bacterium and the ceech inhibitor egiln. C. ...

I. Acta Civeriallog: B. 47.77.2-730(1991).

- I CATALYZES THE HYDRCXXXIS OF PROTEINS AND PEFTIDE AMIDES.

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- CATALYZES THE HYDRCXXXIS OF PROTEINS AND PEFTIDE AMIDES.

- CATALYZES THE HYDRCXXXIS OF PROTEINS AND PEFTIDE AMIDES.

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- CATALYZES THE HYDRCXXXIS OF PROTEINS WITCH DICAG Specificity and PALL AMISCELLULM LONGER PROTEINS WITCH BLOCK SPORULATION AT EARLY SPORULATION, AND MANY MUTATIONS WHICH BLOCK SPORULATION AT EARLY STREED AND PEFTIDASE FAMILY SB; ALSO KNOWN AS THE SUBTILIARSE FAMILY: BELLOGRS TO PEPTIDASE FAMILY SB; ALSO KNOWN AS THE SUBTILIARSE PAMILY.
"complete amino acid seguence of alkaline mesentericopeptidase; subtilisin isolated from \beta strain of Bacillus mesentericus."; FEBS Lett. 196:228-232(1885).
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PDB; IMEE; 15-JAN-93.
MEROPS; S08.002; -.
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01-FEB-1995 (Rel. 31, Created)
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15-JUL-1998 (Rel. 35, Last senote
N-protease (EC 3.4.21..)
Bacillus sp. (Strain KSM-KA6)
Bacteria; Firmicutes; Bactilus/Cl
Bacillus/Staphylococcus group; Re
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                                                                                                 EMBL: M28537; AAA87324.11.
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Q99405; IMPT.
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DT 15-JUL-1995

DE N-PTOCEASE

OS BACILLUS SP.

C BACILLUS SP.
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SEQUENCE
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                                                                                                                                                                                                                                                             142 VSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDD-GGH 200
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                                                                                                                                                                                                                                                                                                                                           120 DVINNSLG---GPIGSTALKTVVDKAVSSGIVVAAAAGNEGSSGSTSTVGYPAKYPSTIA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 VGAVNSANORASFSSAGSELD-----VMAPGVSIQSTLPGGT-----YGAYNGTS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATPHVSGVGALILQAHPSHTPDKVKTALIETADIVAPKEIADIAYGAGRVNVYKA 434
                                                                                                                                                                                                                                                                                 'sal Y.-C., Lin Y.-T., Li Y.-F., Yamasaki M., Tamura G.,
Characterization of an alkaline elastase from alkalophilic Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDNEG-2670913; MEDLINE-89359181; PubMed-2670913; Manako R., Koyama N., Tsai Y.-C., Juang R.-Y., Yoda K., Yamasaki M.; Molecular cloning of extructural gene for alkaline elastase YeB, a new subtilisin produced by an alkalophilic Bactilus strain."; J. Bacteriol. 171:5232-5236(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAS A SUBSTRATE PREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                    Query Match
14.5%; Score 499.5; DB 1; Length 275;
Best Local Similarity 42.9%; Pred. No. 1.7e-21;
Matches 127; Conservative 37; Mismatches 99; Indels 33.
                                                                                                                                                                            27655 MW; 338DA897DBA4170A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp. (strain YaB).
Bacteria: Firmicutes; Bacillus/Clostridium group:
Bacillus/Staphylococcus group; Bacillus.
NGBI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Alkaline elastase Yab precursor (EC 3.4.11.-).
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-!- FUNCTION: DIGEST ELASTIN EFFICIENTLY.
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the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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14.3%; Score 491.5; DB 1; Length 378;
Best Local Similarity 33.7%; Pred. No 7e-21;
Matches 148; Conservative 2.69; Mismatches 155; Indels 67;
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(strain KSM-K16).
Micutes; Barxilus/Clostridium group;
hylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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6, Last annotation update)
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MEROPS; SOB.103; -
InterPro: IPR000209; Peptidase_S8.
Fram; PF00082; Peptidase_S3: 1
FRUITS; PR00133; SUBTILiss.N.
PROSITE, PS00136; SUBTILiss.HIS; 1
FROSITE; PS00138; SUBTILiss.HIS; 1
FROSITE; PS00138; SUBTILiss.SE_SER;
Hydrolase; Sefine Protease; Sumogen; Signa
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102 THVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYGIR 261
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                                                             new alkaline serine protease (M-protease) from
                                                                                                                                        Y., Adachi S., Hitomi J., Yoshimatsu T.
                                                                                                                                                                    properties of an alkaline protease from
                                                                                                                                                                                                                                                                                                                                                                                                             7A03C86D534A1D07 CRC64;
                                                                                                                                                                                    us sp. KSM-K16.";
(otechnol. 43:473-481(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 6.84
43; Mismatches
                                                                            cillus sp. KSM-K16.";
ta crystallogr. D 51:199-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.4%
Matches 122; Conservative
NCBI_TaxID-1409;
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SEQUENCE
  SOTETTE
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Search completed: October 31, 2002, 13:30:07 Job time : 15 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

October 31, 2002, 13:25:48 ; Search time 29.5 Seconds (2) (without alignments) 3864.531 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-841-553-1 3437 1 HKRLGAVVLALVLVGLLAGT.......XAYSTYGWADYQLKAVVYKG 659

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

562222 seqs, 172994929 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vartebrate:*
sp_unclassified:* SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_nammal:*
6: sp_nammal:* ap_mhc:* ap_organelle:* ap_phage:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMNARIES

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Š.	Score	Match	Match Length DB	03	ID OI	Description
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                                                                                                                                                                                                                                                                                                                                                    SQVIAGMEWAADQ----GADVVNMSLGSSGATDGTDPMSQALNDLSRRTGTLFVVAAGME 371
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                                                                                                                               RDRAVKVLELMGAQV------KYSYKIIPAVAVKIKARDLLLIAGMIDTGYFGUTRY 122
                                                                                                                                                                                                                         123 SGIKFIQEDYKVQVDDATSVSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVI182
                                                                                                                                                                                                                                                                      GWYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVN-SQYIGVAPGAKLVGVKVLGADGSGSV 24/1
                                                                                                                                                                                                                                                                                        372 GEGGPRIVGSPGAADAALIVGAVDRDDSLAPFSSRGPRLGDDAVKPDVIAPGVGIVAARA 431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1245;
                                                                                               pred. No. 6e-28;
67; Mismatches 134; Indels
                                             74EE92DB9CAlDE60 CRC64;
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                                                                            20.3%; Score 699; DB 2
41.1%; Pred. No. 6e-28;
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00137; SUBTILASE_HIS; UNKNOWN_1.
PROSITE; PS00138; SUBTILASE_EER; 1.
SEQUENCE 1245 AA; 130895 MW; 74EE92DB9C
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                                                                                           Best Local Similarity 41.1 Matches 175; Conservative
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Lee S.M., Levine A., Liu B., Masuda S., Mauel C., Medigue C.,

Ra Medina N., Mellado R.P., Mizuno M., Noestl D., Nakai S., Noback M.,

Ra Noone D., O'Relly M., Ogawa K., Ogivara A., Ondega B., Park S.H.,

Ra Noone D., O'Relly M., Portitelle D., Porwollik S., Prescott A.M.,

Rager M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,

Rato T., Scanlan E., Schleich S., Schroeter R., Scolfone F.,

Sato T., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

Satouth M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,

Tosaco V., Uofiyama S., Vandenbol M., Vaniher P., Tognoni A.,

Viari A., Mambutt R., Weller E., Weller H., Weltzenegger T. Yata K.,

A Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

The complete genome sequence of the gram-positive bacterium Bacillus

The Lander R., Danchin A.,

The complete genome sequence of the gram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 AGVDWVVQ-NKDK--YGIRVINISLGSS---QSSDGTDSLSQAVNNAWDAGIVVCVAAGN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGPNTYTVGSPAAASKVITVTAVDSN-----DNIASFSSRGPTADGRLKPEVVAPGVD 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5% Score 669.5; DB 16, Length 46.0%; Pred. No. 5.2e-27; ive 51; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299113; CAB13610.1; ***
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01-027-2000 (TrENBLrel. 25, Last sequence update)
01-0EC-2001 (TrENBLrel. 35, Last annotation update)
1NTRACELLULAR ALKALINE SERVE PROFESSE.
APRX OR BH1930.
Bacillus halodurans.
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InterPro: IDR000209; Peptidase_S8.
Pfan; PR00723; SUBTILESIN,
PROSITE; PS00136; SUBTILESIN,
PROSITE; PS00137; SUBTILESE, ASP; 1.
PROSITE; PS00137; SUBTILESE, ASP; 1.
PROSITE; PS00138; SUBTILESE, ASP; 1.
PROCESSES, COMPLETE PS00138; SUBTILESE, SER; 1.
PROCESSES, COMPLETE PS005, WA; B996446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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PRELIMINARE.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.5%; Score 637; DB 16; Length 444; 39.2%; Pred. No. 2.48-25; 1.48-68; Mismatches 122; Indels 36; Gags 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 QVKYSYKIIPAVAVKIKARDL--LLIAGMIDTGYFGNTRVSGIKPIQEDYKVQVDDATSV 142-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 OLRHSFSKIRCVSANVIPESLOEMLVCKDIRKIY------LNREVHALLDTAVES 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 VITVGAVD-----SNDNIASFSSRGPIADGRLKPEVVAPGVDIIAPRASGT----SM 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 SQIGADTVWNSLGYDGSGYVVALVDIGIDANHPDLKGKVIGWYDAVNGRSTPYDDGSHGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 AQ-APEVIRNGETLTGKDYTIAVIDTGI-YPHEDLEGRIKAFVDFVNQREEPYDDNGHGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 HVAGIVAGTG-SVNSOYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKY----258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 GIRVINLSLGSS---QSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 GTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
50-BDC-2001 (TrEMBLrel. 19, Last annotation update)
50-BTILLSIN-LIKE PROTES.
51-STEPTOMYCES albogiseolus.
51-STEPTOMYCES albogiseolus.
62-CETOMYCES STEPTOMYCES: Actinobacteridae;
63-CHOMYCES STEPTOMYCES STEPTOMYCES
                                                                                                                                                                       *Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis, a. Nucleic Acids Res. 28:4317-4331(2000).
ENBEL APOUISI3; BAB05649.1; -. HSSP; 099405; IMPT.
                                                                   SEQUENCE FROM N.A.
STRAIN-C-125 / UCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuli P., Hirama C., Nakamura T., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                    Protease, Complete proteome.
SEQUENCE 444 AA; 48916 MW; 3805F81C53A21F2F CRC64;
Bacteria: Pirmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus,
NCBL_TaxID-86665;
                                                                                                                                                                                                                                                                         InterPro: IPR001128; Cyt_P450.
InterPro: IPR001029; Peptidase_S8.
InterPro: IPR00223; Peptidase_S8.
PRINTS: PR00723; SUBTILISIN.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWH_I.
PROSITE; PS000136; SUBTILIASE_ASP; UNKNOWH_I.
PROSITE; PS00136; SUBTILIASE_HIS; II.
PROSITE; PS00138; SUBTILIASE_HIS; II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 39.29
Matches 146; Conservative
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118 GNTRVSGIKFIQED--YKVQVDDATSVSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHP 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGADGSGSVSTIIAGVD##W-NKDKYGIRVINLSLGSSQSSDGTDSLSQAVNN-AWDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 VVCVAAGUSGPHTYTVGSPAAASKVITVGAVDSNDNIASFSSRGP-TADGRLKPEVVAPG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 VDIIAPRASGTSMGTPINOY---YTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTAL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 VDITAASAKGNDIAKEVGGTXVAGYTVAGTSHATPHVAGAALLKQOHPEWKYAELKGAL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 TASTKD----GKYTPFEQGEGRYQVDKAITQTVIAEPVSLSFGVQQWPHADDKPVTKKLT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 F----TGSVADKGSATHT: ...----FDVSGATFVTATLYWDTGSSDIDLYLYDPNGN 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 EVDYSYTAYYGFEKVGYYNFŢACTWTVKVVSY------KGAANYQ------ 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576 AVDCTYSAYVVATGAGOSVA? AAVEREVESYNVTLKVLDRSCKATANYMAYLSGLTGLG 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32,22; Prod. No. 8.96-25; Matches 201; Conservative 772; Mismatches 219; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 YRNLGTEDVTLKLTSTATGOKGKAAPAGFFTLGASTLTVPA---NGTASVDVTADTRLGG
STRAIN-S-3253;
MEDLINE-97144528; PubMed-9990295;
Suzuki M., Taguchi S., Manada S., Kojima S., Miura K., Momose i Suzuki M., Taguchi S., Siziki III and Stroptomyces alogriseolus."
Stroptomyces alogriseolus."
Embl., D37672; BAB12440.1.
EMBL, D37672; ASB12440.1.
HSSP: P00782; 2587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18:5%; Score 636; DB 2; Length 1102; 32.7%; Pred. No. 8.9e-25;
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                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0723; SUBTILISIN.
PROSTE: PSO0136; SUBTILISE. ASP: UNKNOWN.1.
PROSTE: PSO0137; SUBTILIASE. ASP: UNKNOWN.1.
PROSITE; PSO0138; SUBTILIASE.ERR: 1.
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                                                                                                                                                                                                                                        InterPro: IPR002860: BWR
InterPro: IPR000209: Peptilase_SB
Pfam: PF02012: BNR: 2
Pfam: PF00082: Peptidase_S8: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 VDRSTSSNSYEHVEYANPARCTWT 636
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260 IRVINISIGSSQSSDGTDS). SCAVNN-AWDAGIVYCVAAGNSGPNTYTVGSPAAASKVIT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 GIHVAGIVAGIGSV-NSQYKGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGAVDSNDNIASFSSRGP" GGSRLKPEVVAPGVDIIAPR---ASGTSMGTPINDYYTKA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGAVDSADQAAWETSAGPRECONALKPDLSAPGVGILAARSRLAEGSG------DYTSM 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 PYLRDGSLDERLFDVGAL EQGLA-----DSETGELPLIVTYG---KGVRAATPRGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERTRSLPSVRGAAVE-----ADKGRAFWREFTRRGAGVEGVWLDGRVTADMAE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 PVVRNNAVQQKNY---GLETPPCLFKKVQRMNWNQEVDTVIMFGSYGDRDRAVKVLRLMGA 84
                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Ripswood D.A.; "A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1956).

BMB: All63003; CA886111.1; "RBE: A165903; CA886111.1; "RBE: A165905; IMPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCTSMATPHYSGVGALILQAEPSWTPDKVKTALIETADIVAPKEIADTAY - - GAGRVNVY
                                                Streptomyces coelicolor: Streptomyces coelicolor: Streptomyces, Actinobacteria; Firmicutes; Actinobacteria; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAIKYDDYAKLTFTGSVADKGSANHTFDVSGATFVTATLYWDTGSSDIDLYL 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1220;
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Best Local Similarity 36.4%; Pred. No. 4.8e-24;
Matches 172; Conservative, 851; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                               Cerdeno A.M., Parkhill d., Rarrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TherPro; 1PR003137; PA.
InterPro; 1PR003137; PA.
InterPro; 1PR00209; Peptidase_S8.
Pfam. PPC0225; PA: 1.
PR00122; PA: 1.
PR00123; PA: 1.
PR00125; PA: 1.
PR001E; PS00136; SUBTILESE_NE; UNKNOWN_1.
PR005IE; PS00136; SUBTILESE_NE; UNKNOWN_1.
SEQUENCE 1220 AA; 127311 MW; B9BD0018A7F31674 CRC64;
                                                                                                                                                                                                           Brown S.P., Harris D.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
MEDLINE-97000351; PubMed*E843436;
                            PUTATIVE SECRETED PEPTIDASK.
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                                                                                                                                                                                              STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 QGHGTHVAGIVAGTG-SVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYGIRVINLSLGSSQS-SDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASK 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AITVGAVDDKRIPDIEDDEVAKFSGRG--GPYLYKPDVVAPGVKIVSTASGNVPFGADET 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 -INDYYTKASGTSMATPHVSGVGALILQABPSWTPDKVKTALIETADIVAPKEIADIAKG (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVSQ1GADTVWNSLGYDGSGVVVAIVDTGIDANHPDL---KGKVIGHYDAVNCRSTPYDD. 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%; Score 633; DB 2; Length 412;
41.5%; Pred. No. 3.5e-25;
tive 52; Mismatches 129; Indels 36; Gaps
                                                                                                                                                                                                                                                 Jang H.J., Kim B.C., Pyun Y.R., Kim Y.S.;
"A novel subtilisin-like serine protease from Thermoanaerobacter yonseiensis KB-1: cloning, expression and blochemical properties." Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Jang H.J., Klm B.C., Pyun Y.R., Kim Y.S.;
"Subtiliain-like protease, thermicin, from Thermoanaerobacter
Yonseil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Volbalited (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AT028704; AAK27733.1; --
EMBL; AF05633; AAL09366.1; --
EMSP; Q46670; 1DBJ.
InterPro; IPR000209; Peptidase_S8.
Priam; PF000082; Peptidase_S8.
PRINTS; PR00723; SUBTILISIN.
PROSTITE; PS00134; SUBTILIASE_EMB; IPROFITE; PS00137; SUBTILASE_EMB; IPROFITE; PS00137; SUBTILASE_EMB; II.
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SEQUENCE 412 AA; 44503 MW; E3C6AOFB1B1A1D47 CRC64;
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01-JUN-2001 (TERBIRE). 17, Last sequence update)
01-DEC-2001 (TERBIRE). 19, Last annotation update)
THERMICIN (SUBTILISIN-LIKE PROTEASE THERMICIN).
                                                                                                                              Thermoanaerobacter yonsell.
Bacteria: Firmicutes: Bacillus/Clostridium group;
Breferia: Firmicutes: Bacillus/Clostridium group;
RCBI_TaxID=111519;
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524 GAAN----YOVDVVSDGS 537
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STRAIN-A3(2):
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Runahl H., Hopwood D.A.;

* A set of crdered cosmids and adetailed genetic and physical map for

the 8 wb Streptomyces coelicolor A3(2) chromosome.*;

Runcreptor in Prof. 1777-96(1996).

Runcreptor in Prof. 1777-96(1996).

Runcreptor in Prof. 1777-96(1996).

Robertor in Prof. 1777-96(1996
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|PGVGVLAARSRYAPEG---EGAYOSLSGTSWATPHVAGAALLAAEHPDWTGQRLKEALV 467;
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                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria: FirmLoutes: Actinobacteria: Actinobacteridae;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
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Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE SECRETED PEPTIDASE.
                                                                               PRT; 1253 AA
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MEDLINE=97000351; PubMed=8843436;
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STRAIN-A3[2];
REDLINE-3700351;
Redenbach M., Kloser II.M., Denapaite D., Elchner A., Cullum J.,
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces cosmids and a Mb Streptomyces cosmids with a Mb Streptomyces cosmids and a Mb Streptomyces Casilcolor A3(2) chromosome.";
EMBL, A1391041; CAC01588 1, ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 IDANHPDLKGKVIGWYDAVNJRSTPYDDQGHGTHVACIVAGTGSVNS-QYIGVAPGAKLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 VDAGHPDLADRIAARQSFV3E3WTD-DRDGHGTHVASTIAGTGAASAGKEKGVAPGARLS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 GVKVLGADGSGSVSTIIAG%LV-VOOKDKYGIRVINLSLGSSGSSDGTDSLSGAVNN-AW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 DAGIYVCYAAGNSGPNTYGVUDAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 APCVDIIAPRASGISMGIPZEDZITKASGISMAIPHVSGVGALILQAHPSWIPDKVKTAL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
Barceria; Winkoubes; Actionacteria; Actinobacteridee;
Actinomycetales; Streptomycetaceae; Streptomyces.
NCBL_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.2%. Score 590; DB 2; Length 1239
Best Local Similarity 32.1% Pred. No. 2.4e-23;
Matches 172; Conservative 74; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DobJ databasas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003137; PA.
InterPro; IPR002109; Profitionse_S8.
InterPro; IPR00229; Pa; 1.
Pfam; PR00028; Papt 1.
PRINTS: PR00723; SUBTILISIN.
PROSITE: PS00136; SUBTILISIN.
SEQUENCE 1239 AA: 1.3505 MM; BF5E9AC68B1260A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                              09FB34;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE_SECRETED PEPTIBASE.
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SEQUENCE
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                                         316
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09F942
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STRAIN—OND 1411.

STRAIN—OND 1411.

Glodateln G., Waspaner E.K., Lee Y.E., Masisak E.S., Oh J.;

Glodateln G., Waspaner E.K., Lee Y.E., Masisak E.S., Oh J.;

Nucleotide sequence of kerA gene encoding a keratinolytic protesse of Bacillus licheniformis own 14117.

Bacillus licheniformis own 14117.

EMBL; AF282893; A6300421.

EMBL; AF282893; A6300421.

EMBL; AF282893; A6300421.

FINSE; PRO738; SUBTILISIN PRO1315; SUBTILISIN PROSTIE; PRO1316; SUBTILISIN PROSTIE; PRO1316; SUBTILISIN DC65F6A93EBC69CC CRC64;

SEQUENCE 379 AA: 38904 MW; DC65F6A93EBC69CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 ---VEEDHVAHALAQIVYYGIPLIKADKV-QAQGYKGANVKVAVLDTGIQASHPDL: NV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 IGWYDAVNGRSTPYDDOGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGLGSV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 STIIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAF3%SG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 SGIVSGIEMATIN----GMDVINMSLG---GFSGSTAMKGAVDNAYARGYVVVAAAGKSG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 P.-NIYIVGSPAAASKVIIVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAFRAS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 IKFIQEDYXVQVDDAT---SVSQIGADTVWNSLGTDGSGVVVAIVDTGIDANHPDL::GKV: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GSYGDRDRAVK--VLRLMGAQVKYSYKITPAVAVKIKARDLLLIAGMIDTGYFGNTRVSG 124
                                                                                                                                                                                    573 HGTAD -- VILIIDGSGSAGG-------RAISGGIL----ATDADARN'A GOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 GATEVTATLYMDIGSSDIDLYLYDPNGNEVDYSITAYYGFEKVGYYNPIAGIWIVKVVSY 522
                                                                                                                                                     523 KGAANYQVDVVSDGSLSQSGGUPNPNPNPNPTTTDTQTFTGSVNDYWDTSDTFTMNVN 582
                                                                                                                        539 NTTGAAVTL.....572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYLALVLVGELAGTALAAPVKPVVRNNAVQQKNYGLLTPGLFKKVORMNHNOEVDTVINF 68
429 APGYGILAANSSFAAGG---NGAYQSLSGTSMATPHYAGAAALLAAARPDLSGSALK--- 482
                              108 IETADIVAPKEIADIAY----GAGRVNVYKAIKYDDYAKLIFTGSVADKGSATHTFDVS 462
                                                          483 ----DVLASSSHRIPRYDARQAGSGRYDYDAAVRAGVYASATAYAPGSSPGPVRRLVTYT 538
                                                                                                                                                                                                                                     HTAVS-AGPVR-----HKLTVHFKDADG------NPVPGVFDLL, 6403
                                                                                                                                                                                                                    583 SGATKITGDLIFDTSYNDLDLYLYDPNGNLYDRSISSNSYEHVEYANPAPGIWTFL 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.4%; Score 564.5; DB 2; Length 3
35.6%; Pred. No. 1.1e-21;
iye 61; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus licheniformis.
Bacillus/Clostridium group:
Bacillus/Staphylococcus group: Bacillus/Staphylococcus group:
                                                                                                                                                                                                                                                                                                                                  379 AA
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 35.68
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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09FDF4
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P--NIYIVGSPAAASKV: "VGAVDSNDNIASFSSRGPIADGRLKPEVVAPGVDIIAPRAS 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STIIAGVDWVVQNKDKYGINVINESLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 SSGNINITGYPAKYDSVIA:75kVDSNSNRASFSSVG-----AELEVIAPG------A 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 IKFIQEDYKVQVDDAT---SVSUJGADTVWNSLGYDGSGVVVAIVDIGIDANHPDLKGKV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSYGDHDRAVK -- VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGHIDIGYFGNTRVSG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VYLALVLVGLLAGTALAAPV#FFVVRNNAVQQKNYGLLTPGLFKKVQRMNNQEVDTVIMF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
360 GISMGTPINDYYTKASGISMATÇHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-NCIMB 10689;
MEDLING-20561774; Pubmed-11109488;
Evans K.L., Crowder J.S.; Maller E.S.;
"Subtilisins of Bacillus 272, hydrolyze keratin and allow growth
                             ST-----YATLNGTSKASPAVAGAAALILSKHPNLSASQVRNRLSSTAIYLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.1%; Pred. No. 1.2e-21;
Matches 156; Conservative 61; Mismatches 140; Indels 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 374 374 374 374 B61432A1B42C526E CRC64;
                                                                                                                                                                                                                                                                                            01-WAR-2001 (TrEMBLrel. 16; Created)
01-WAR-2001 (TrEMBLrel. 16; Last sequence update)
01-DEC-2001 (TrEMBLrel. 19; Last annotation update)
SUBFILISIN PRECURSOR (EC. 3:4.21.62) (FRAGNENT)
                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus licheniformis.
Bacteria, Pirmicutes; Banillus/Clostridium group;
Bacteria, Firmicutes; Banillus/Clostridius.
Bactilus/Staphylococcus group; Bacillus.
NCBL_TaxID-1402;
                                                                                                                                                                                                                                                       374 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Can. J. Microbiol. 46:1064-1011(2000).
EMBL: AP205190; AAC310273 3374.
HSSP: P00780; 1CSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interproj IPRO02099, Pepthydae_58.
Pfam; PRO0082, Peptidase_28; 1
PRINTS; PRO0723; SUBTILISIN.
PROSITE; PS00136; SUBTILISIN.
Signal; Hydrolase.
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                   363 SSFYYGKGLINVEAA 377
                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                  420 ADIAYGAGRVNVYKA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-NCIMB 6816,
STRAIN-NCIMB 6816,
BUDLINE-20561734; Pubmed-11109488;
Evans K.L., Crowder J.S., Miller E.S.;
Subtilisins of Bacillus spp. hydrolyze keratin and allow growth on
308 GVYSTYPTNTYAT-LNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATYLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 NQEVDTVIMEGSYGDRDRAVK--VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGNID: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 GYFGNTRVSGIKFIQEDYKVQVDDAT---SVSQIGADTVWNSLGYDGSGVVVALVDTG1D-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 ANHPOLKGKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGIGSVNSQYIGVAPGAKLVGVK: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 VLGADGSGSVSTIIAGVDHVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 VVCVAAGNSGP--NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.4%; Score 562.5; DB 2; Length 374;
39.0%; Pred. No. 1.3e-21;
tive 54; Mismatches 130; Indels 49; Gago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 AY------VBEDHVAHALAQTVPYGIPLIKADKV-QAQGFKGANVKVAVLDTGIQ:141
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CHAIN 30 >374 SUBTILISIN.
NON_TER 374 374
SEQUENCE 374 AA; 38396 MW; 6046C17B985413B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2001 (TrENBLrel. 16, Created)
01-WAR-2001 (TrENBLrel. 16, Last sequence update)
01-DEC-2001 (TrENBLrel. 19, Last annotation update)
SUBTILISIN PRECURSOR (EC 3.4.21.62) (FRAGNENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacilius licheniformis.
Bacilius Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                      374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Can. J. Microbiol. 46:1004-1011(2000).
EMBL: AF705189: AAG31026.1:
INTERPO. 1CSE.
INTERPO. 1PR000209; Peptidase_S8.
Pfam: PF00082; Peptidase_S8: 1.
PRINTS, PR00729; SUBTILISIN.
PROSTTE; PS00136; SUBTILIASE_ASP: 1.
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Best Local Similarity 39.00
Matches 149, Conservative
                                                                              420 ADIAYGACRUNY 431
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363 SSFYYGKGLINV 374
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94 AY------VEEDHYA!ALAQTVPYGIPLIKADKV-QAQGFKGANYKYAVLDTGIQ 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 VLGADGSGSVSTIIAGVDRVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 VVCVAAGNSGP--NTYTVGSPAASKVITVGAVDSNDNIASPSSRGPTADGRLKPEVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 GVDIIAPRASGISMGTPINDYYTKASGISMATPHVSGVGALILQAHPSWTPDKVKTALIE 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.74; Pred. No. 1.94-21;
Matches 149; Conservative 54; Mismatches 133; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 NOEVDIVINFGSYGDRDRAUK - VLRLMGAQVKYSYKIIPAVAVKIKARDLLIAGNIDT 114
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MEDLINE-95266828; PubMed-7747965;
MEDLINE-95266828; PubMed-7747965;
Ind X., Relemen D.W., Miller E.S., Shih J.C.;
"Nucleotide sequence and expression of kerA, the gene encoding keratinolytic protease of Bacillus licheniformis PWD-1.*;
PAPPL ENTION, Nicrobiol. 62:1469-1474(1995).
EMBL: S78166; ABB34259_1.*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEROPS; SOB.001, Particles.

InterPro: IPR002029; Papticles.

PERM: PR00723; SUBTICIEN;

PRINTS; PR00723; SUBTICIEN;

PROSTEE; PS00136; SUBTICASE, ARP; 1.

PROSTEE; PS00137; SUBTICASE, HIS; 1.

SEQUENCE 379 AA; 38923; MW; 507E2409FIADFE03 CRC64;
01-NOV-1996 (TrEMBLrel, 22) Created)
01-NOV-1996 (TrEMBLrel, 22) Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
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01-WAR-2001 (TrEMBLrel, 16, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
SUBTILISIN PRECURSOR (Fr. 3, 21.62) (FRAGMENT).
Bacillus licheniformis:
                                                                                                                                Bacillus licheniformis.
Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacteria, Firmicutes; Bacillus/Clostridium group;
Bactilus/Staphylococcus/group; Bacillus.
NCBI_TaxID-1402;
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Q9F941
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166 VDTG1DANHPDLKGKVIGWYDÄVNGRSTPYDDOGHGTHVAGIVAGTGSVNSQYIGVAPGA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 AWDAGIYVCYAAGNSGP--NTYTYGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 PEVVAPGVDIIAPRASGTSMSTRINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 GY-----FGNTRVSGIRRIQEDYKVQVDDATSVSQIGADTVWNSLGYDGSGVVVAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan F.W., Chen S.T., Chief S.H.; Sequence characterization of the precursor of one mutant subtillsin from Bacillus licheniforsize (*)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 NQEVDTVIMFGSYGDRDRAVK- VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-11594;
Pan F.M., Chen S.T., Chiou S.H.;
Sequence characterization of the precursor of one mutant subtilisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.2%; Score 556.5; DB 2; Length 379;
Best Local Similarity 38.4%; Pred. No. 2.7e-21;
Matches 150; Conservative 56; Mismatches 130; Indels 61
                                                                                             from Bacillus licheniformis; ;; Submitted (SP-1995) to the EMBL/GenBank/DDBJ databases. EMBL, 91260; CAA2666.1; ... HSSP; POO780; ICSE. MEROPS; SOB.001; ... MEROPS; SOB.001; ... Interpro; IPRO00209; Peptidase_SB. Pfan; PF00082; Peptidase_SB. Prints: PR00723; SUBTILISTE. PR057TE; PS00136; SUBTILISTE. PR057TE; PS00136; SUBTILIASE_HS; I. PROSTTE; PS00137; SUBTILIASE_HS; I. PROSTTE; PS00138; SUBTILIASE_HS; I.
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CHAIN 107 379 POTENTIAL.
SEQUENCE 379 AA; 35082 NW; DEFFECTFREECRASB CRC64;
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01-NOV-1996 (TrEMBLrel. G: Treated)
01-NOV-1996 (TrEMBLrel. 01, List sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SUBSTILISIN CARLSBERG PRECURSOR.
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Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacteria, Firmicutes; Bacillus/Craphylococcus group; Bacillus
NCBL_rexID=1402;
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STRAIN-14353;
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SEQUENCE FROM N.A.
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16.2%; Score.558.5; DB 2; Length 374;
Best Local Similarity 36.1%; Pred. No. 2.1e-21;
Matches 157; Conservative 60; Mismatches 137; Indels 81; Gaps 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 VSGIKRIQEDYKVQVDDAT---SVSQIGADIVWNSLGYDGSGVVVAIVDTGIDANHPHLK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 INFGSYGDRDRAVK--VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFGNTR,121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 GSYSGIVSGIEMATIN----GMDVINMSLG---GASGSTANKQAVDNAYARGVVVVAAAS 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 VGFKS-GVKTASVKKDIIKESGGKVDKQFRIINAAKAKLDKEALKEVKNDPDVAY-----95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC12759;
MEDLINE-20561724; PubMed-11109488;
Evans K.L., Crowder J.S., Miller E.S.;
"Subtilisins of Bacillus spp. hydrolyze keratin and allow growth on
                                                                                                                                                                                                                                                                                                                                                                                                  374 AA; 38423 NW; 640142EB813D0E60 CRC64;
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01-NOV-1996 (TIEMBLIEB. 01, Last sequence update)
01-DEC-2001 (TIEMBLIEB. 19, Last annotation update)
SUBSTILISIN CARLSBERG PRECURSOR.
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Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1402;
Bacterla; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
WCBL_TaxID-1402;
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SUBTILISIN.
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Can. J. Microbiol. 46:1004-1011(2000).

ENEL, AF205191; A631028-1; --
HSSP; P00780; 1CSE.
FIGHERPC; IPRO00209; Peptidase_S8.
Fram; FP00082; Peptidase_S8: 1
PRINTS; PR00723; SUBTILISIN.
SIGNAL; Hydrolase.
SIGNAL; Hydrolase.
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363 ---SSFYYGKGLINV 374
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57 NOEVDTVIMEGSYGDRDRAVK--VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDT 11.4
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/ Pred. No. 5.6e-21;
55; Mismatches 132; Indels 49;
 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
C655CC14A16C1449 CRC64;
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                                                                     Peptidase_S8
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379 PC
38925 MW;
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Best Local Similarity 38.7%;
Matches 149; Conservative 55
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Search completed: October 31, 2002, 13:31:14 Job time : 35.5 seca Teraprese.

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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Archea: Eurysrchaeota; Thermococci; Thermococcales;
Thermococcaeea; Pyrococcus.
1 (base 1 to 12452)
Maeder.D.L., Welss.R.B., Dunn,D.M., Charry,J.L., Gonzalez,J.M.,
DINUgiaro,J. and Robb.F.T.
Divergence of the hyperthermophilic archaea Pyrococcus furiosus and
P. horikoshi inferred from complete genomic sequences
Genetics 152 (4), 1.99-1305 (1999)
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Robb.F.T., Naeder,D.L., Brown,J.R., DiRuggiero,J., Stump,M.D.,
Yeh,R.K., Welse,R.B. and Dunn,D.M.
Genomic sequence of hyperthermophile, Pyrococcus furlosus:
Implications for physiology and enzymology
Meth. Enzymol. 330; 134-157 (2001)
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1306 AAGTACGACGACTACGCCAAGGTCACCTTCACCGGCTCGGCCGACAAGGGAAGCGCC
                          Weiser R.B.
Direct Submission S.
Submitted (12.P29.2) Human Genetics, University of Submitted (12.P28.2) Submitted (12.P28.2) South 2030 Bast, Salt Lake City, UT 84112, USA Location/Qualifiers
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Welse, B., Dunn, D.M., Robb, P.T. and Brown, J.R.
The complete sequence of the Pyrococcus furiosus
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llarity 63.6%; Pred. No. 1e-85;
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/gene-"pF1565"
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5345. An1
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/gene="PF1658"
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<u>a</u> 6	61	GCCCTTGCGGCACCCGTAAAACCGGTTGTCAGGAACAACGCGGTTCAGCAGAAGAACTAC_120
÷ 8	121	GGACTGCTGACCCCGGGACTGTTCAAGAAGTCCAGAGGATGAACTGGAACCAGGAAGTG 180
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S 8	241	CTCATGGCGCCCCAGGTCAAGTACTCCTACAAAATCCCTGCTGCGGGGTTAAAAT 300
ò	30	A 360
đ	11987	
ð	361	AGGGTCTCGGGCATAAAGTTCATACAGAGGATTACAAGGTTCAGGTT
g	11939	AGCTITCAGGTGTAGGTTATCCAGGAAGACTACAAAGTTACAGTTTCAGCAGAATTA 11880
ò	409	GACGACGCCACTTCCCTGCTAGGGGCCGATACCGTCTGGAACTCCCTCGGC 465
9	11879	GAAGGACTGGATGAGTCTGCAGCTCAAGTTATGGCAACTTACGTTTGGAACTTGGGA 11823
ò	46	525
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8 6	11762	GAICTEAAGGGCAAGGTCATAGGGTGGTACGACGCCGTCAACGGCAGGTCGACCCCTAC 585
6	586	6
6 6	9 0	CATGTAGCTTCAATAGCAGCTGGTACTGGAGCAGCAAGT
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8	11582	GCCGATGGTTCTGGAAGCATATCTACTATAATTAAGGGAGTTGATGGGCCGTTGATAAC 11523
3 8	763	AAGACAAGTACGGGATAAGGGTCATCAACCTCTCGCTCGGCTCCTCCCAAGCTCCGGG 822 1
3	82	GGAACGACTCCCTCAGTCACACACACACACACACACACAC
ි දු	· vo	GETACTGACGCTCTAAGTCAGGCTGTTAATGCAGCGTGGGATGCTTGTTGTG_11403
ò	883	6TCGCCGCCCAACAGCGGCCGAACACCTACACCGTCGGCTCACCGCCGCCGCGGAACAGCGGCGGCGGAACAGCGGCGGC
g	11402	GTTGCCGCTGGAAACAGTGGACCTAACAAGTATACATCGGTTCTCCAGCAGCTGCAAGC
2 8	943	AAGGTCATAACCGTCGGTGCAGTTGACAGCAACGACATCGCCAAGTTCTCCAGCAGG 1002
ò	1003	1062
g	11282	GGGCCAACTGCAGACGCCTTAAGCCTGAGGTTGTTGCTCCAGGAAACTGGATAATT 11223

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGCCCACCCGAGCTGGACCCCGGACAAGGTGAAGACCGCCCTCATCGAGACCGCGA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719
                                                                                                                                                                                                                          LOCAL SINIMATERLY 00.01; FIEU. NO. 6.78701; Indels 3; Gaps. 796; Conservative 0; Mismatches 371; Indels 3; Gaps. 659 CCTCGGCTACGACGGAAGCGGTGTGGTGGTTGCCATACGGGTATAGACGCGAA 518
                                                                                                                                                                                                                                                                                                                                        579 CCCCTACGATGACCAGGGACACGGAACCCACGTTGCGGGTATCGTTGCCGGAACCGGCAG 638
                                                                                                                                                                                                                                                                                                                                                                                                                              696 TCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGT (755)
                                                                                                                                                                                                                                                                                                                                                                                                                                             876 AGTCTGCGTCGCCGGCAACAGCGGGCCGAACACCCTACACCGTCGGCTCACCCGCCGC $35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936 CGCGAGCAAGGTCATAACCGTCGGTGCAGTTGACAGCAACGACAACATCGCCAGCTTCTC 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTIGGGATATGATGGTTCTGGAATCACAATAGGAATAGACACTGGAATTGACACTGGAATAGACATTGATTA
                                                                                                                                                                                                                                                                                              CCACCCGATCTGAAGGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGAC_578
                                                                                                                                                                                                                                                                                                          110 TCATCCACATCTCCAAGGAAAGTAATTGGGTAGATTTTGTCAATGGTAGGAGTTA, 179
                                                                                                                                                                                                                                                                                                                                                        816 CTCCGACGGAACCGACTCCCTCAGGCCGTCAACAACGACGCCTGGGACGCCGGTATAGT 875
                                                                                             1 (bases I to 1236)
Takakura, H., Mortshitt, M., Shimojo, T., Asada, K. and Kato, I.
Themostable protease
Patent: US 6358726-A 2 19-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                  1056 CATCATAGCCCCCCCCCCCAGCGAACCAGCATGGCCACCCCGATAAACGACTACTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 GATAATTGCTGCCAGAGCAAGTGGAACTAGCATGGGTCAACCAATTAATGACTATTACAC
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                                                                                                                                                                                                          Length 1236;
                                                                                                                                                                                                          Score 560.4; DB 6; Length 1
Pred. No. 2.7e-61;
0; Mismatches 371; Indels
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          1236 bp
from patent US 6358726.
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/organism="unknown"
251 c 309 g
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Sequence 2 from patent (
AR201146
AR201146.1 GI:20252034
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Matches 796, Conservative
                                                                          Unknown.
Unclassified
                                                                 Unknown
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PAT 04-DEC-1998
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Mitta, M., Yamamoto, K., Morishita, M., Asada, K., Tsunasawa, S. and
                                                                                                                                                                                                                     960 AGGCAGCCAAACTCACCAGTTOTTATTAGCGGAGCTTCGTTCGTAGAACTGCCACATATA 1019
                                                                                                                                                                                                                                                                                                                                             1476 TGACTACTCCTACACCGCCTACTACGGCTTCGAGAAGGTCGGCTACTACAACCCGACCGC 1535
                                                                                                                                                                                       1356 GGGAAGCGCCACCCACACCTTCGACGTCAGCGCGCCCACCTTCGTGACCGCCACCTCTA 1415
                                   1236 CATAGTCGCCCCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGGTAGGGTGAACGTCTA 1295
                                                                                                             1296 CAAGGCCATCAAGTACGACGACTACGCCAAGCTCACCTTCACCGGCTCCGTCGCCGACAA 1355
                                                           780 CCAAGCACACCCGAGCTGGAGTCCAGACAAAGTAAAAACAGCCCTCATAGAAACTGCTGA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 CACGGAACCCACGTTGCGGGTATCGTTGCCGGAACCGGCAGCGTTAACTCCCAGTACATA 657
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Pred. No. 9.2e-58;
0; Mismatches 17;
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Hyperthermostable protease gene
Hyperthermostable protease gene
Patent: US 5756339-A 11 26-MAY-1998;
Locatlon/Qualiflers
1. 554 n. 754 n. 754 n. 754 n. 754 n. 151 a 195 n. 161 g 87 t.
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Best Local Similarity 97.05;
Matches 543; Conservative
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binding-protein dependent transport protein; hydrolase; integral
membrane protein, laci family transcriptional regulator;
Mark-family protein, membrane transport protein;
Mark-family protein; membrane transport protein;
pyrrolidone-carboxylate peptidase; secreted peptidase; secreted
protein; secreted solute-binding importotein; SIR2-like regulatory
protein; sugar phosphotransferase; tefk family transcriptional
regulator; transcriptional regulator; transmembrane efflux protein.
Straptomyces coelicolor A3(2)
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescae; Streptomycescae; I (bases 1 to 4352)
Redenbach, M., Kieser, H.M., Denapalte, D., Eichner, A., Cullum, J.,
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Murphy, L. and Rajandream, M.A.
Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Submitted (28-SEP-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@eanger.ac.uk Cosmids supplied by Profer Colney, Norwitch, Norfolk NR4 7UH, UK
On May 9, 2002 this sequence version replaced g1:6002208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCT 12-MAY-2002
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S.coelicolor/) CDS.are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complèmentary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 Wh Streptomyces coelicolor A3(2) chromosome
MOI. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                GGAAGGCTCAAGCCGGAAGTCGTCGCCCCCGGCGTTGACATCATAGCCCCCGCGCGCCCAGC 1077
                                                                                                                                                                        AGCGGCCGAACACCTACACCGTCGCTCACCCGCCGCGGGGGAGCAAGGTCATAACCGTC 957
                                                                                              DNA
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AL121596.2 GI:20520772
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JOURNAL
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REFERENCE
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/gene="SCF51A.01"
/gene="SCF51A.01"
/note="SCF51A.01"
/note="SCF51
in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jun/cgi-bin/firshcip/
Jun/cgi-bin/firshcip/
Correct initiation/Scdon. Where possible we choose an initiation
coon (atg, stg, fig or (atl)) which is preceded by an upstream
ribosome binding site sequence (optimally 5-13bp before the
initiation codon) of if this cannot be identified we choose the most
upstream initiation codon. The sequence of the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions. Cosmid 51A overlaps
cosmid F76 on the Asel-F genomic restriction fragment.
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/translation-wattiricorderrrewytlawaavvlgvvcgamsageagdds
/translation-wattiricorderrrewytlawaavvlgvvcgamsageagdds
SSWSSPLDAATVSQDGSTAYATVTEVTEDWYDDAGRADLTAAVERARTSGLT
VEAGGSAVAGEPPAGIGERIGICOAAVVLLTFSSLAAGLDLTAAVGYALTLASIV
VEAGGSACWATASPAGIGERIGICOAAVVLLTFSSLAAGLAVGYALTLASIV
ALGSALGWSTASDGAAWIGTNGVDYAAVLAVSRRREERAEGIIDARAACAACTAGS
AVFRGITYVIALAGLSVIGVPSLTKWGLAAAGAVVIAVLTTLUVPALGGEWDDALL
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YOYLLIÇSALLIĞALAVRALDIGINIGACOBARRTSTTERRATOLLAGGERGENGELTY
VOYLLIÇSALLIĞALAVRALDIGINIGATAGOVSVRAPPRINAAKOTAVIGAVPARPETTY
VOYLAKQALDDPRSAVAA VSDRLAATAGOVSVRAPPRINAKOTATIOTOVPGITAVIGSETTE
ELVHTINDERHA"ESATGATFEVTGTTALNIDVARKMTDALIPYLLVVVGLAFLILLV
VERSULPÜKÄALLGYGASFGALVIVIRQNGHGAGALLIÇESTGEVMSTWALMIVĞI
VEGLAMLYQÜPINSKARRARVHGERPARAVTGFRBISCRVYTAAANINTSYACAFTG
GETLIKRAYĞĞIAVAYLEDAFVVRMAFVPAVLLICERRAMILPRILDRLLIPRVDVGG
GETLIKRAYĞĞĞIAVAYLEDAFVVRMAFVPAVLLICERRAMILPRILDRLLIPRVDVGG
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/transl_table=11
/product="hypothetical protein SCF51A.02."
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/strain="A3(2)"
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/gene="CCF51A.02"
/note="SCF51A.02, unknown, len: 168 aa."
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/note="SCK0423"
complement
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RD-"Cransletion-"MPGWTAGPTOFFCHGAGRGDFDGPRVSAVPAAQCVEMGPG
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RATRACPASGRSAGTRIASVQVPGPARRSRRPGAVVGAAVPGRFHRAAAGRDDVALAA
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//note="SCF51A.03c"
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Streptomyces coelicolor TR:CAB46385 (ENBL: AL096743)
//pyochetical 30.5 KD protein SCI7.02c (281 as).fasta
scores opt: 42 4 2 - Score: 490.6 E(): 5.7e-20 36.68 identity
in 292 as overlap.
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/td_sslet_on="Betrial Fight Fig
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AAAHEPSLVTAVVELAPPTRKQSVRLGDLRVRRFRRGHLRLLGAGREGSTELAMBSYLD
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protein_id="CAB56656.1"
db_xref="G1:6002212"
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4624. :5295
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/note="Pfam match to entry PF00561 abhydrolase, alpha/beta
hydrolase fold, score 74.40, E-value 2.4e-18"
5332. :5395
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                                                                                                                                                                                                                                                                                                  1267 GCCTACGGTGCGGGTAGUSTGAACG-----TCTACAAGGCCATCAAGTACGACGAC 1317
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Best Local Similarity 54.8%; Pred. No. 1.5e-22;
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                                                                                    1438 ATCGACCTCTACCTCTACGACCCCAACGGAACGAGGTTGACTACTCCTACACCGCCTAC 1497
                                   GACGTCAGCGGCCCACCTTCGTGACCGCCACCTCTACTGGGACACGGGCTCGAGCGAC, 1437
                                                                                                                                    TACGGCTTCGAGAAGGTCGGCTACTACAACCCGACGCGGAAACCTGGACGGTCAAGGTCAAGGTCAA
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Sequence 1 from patent US 6361987.
AR202321
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473 a 1041 c 984 g
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AB007809 100-2002 Streptomyces viridospokus dhpA gene for 1.4-dihydropyridine enentioselective exterase, complete cds. AB007809
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Streptomyces viridosporus
Bacteria; Firmicules: Actinobacteria; Actinobacteridae;
Actinomycetales; Screptomycineae; Streptomyces
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CGGGCGCCCAGTCCAAGGGQAAGTACAAGGGCGTCGCACCCGGCGCCGCGGTCCTCAACG 1223
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                                                                                                                                                                     GGGTCGTCCAGAACAAGGACAAGTACGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCT 808
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LEDRAKBDAGHPLVDAFYTLGEPOTEKAGKKYTKRFWTAVFGPRLSADYGLFRDGNT
LYGLEPLFADGKGHAGSSDFTSATTSLTRNGKKIGSHSDPLLGGDEFYYRAGDST
TYGLESARVAASTRIDASWTFRSKKTTGFTQLPASTVFFGAVTGLDEFYYRAGDSKYTF
FPYTVEGAARGKNLKSLSVYVSYDSGKTWKKTTVTKGKITVKNPAKGKAISFRAKTA
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/product=11,4-dihydropyridine enentioselective esterase"
/protein_id=#AC00500.1"
/db_raef=GI:31322744*
                                                     ted (07-OCT-1997) Akira Arisawa, Bloresource Laboratories, in Corporation; 4-9-1 Johnan, Fujisawa, Kanagawa 251-0057, (E-mail:arisawa-a@mercian.co.jp, Tel:81-466-35-1511,
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/function=potentialtranscription terminator"
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Pred. No. 3.2e-15;
0; Mismatches 439; Indels
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Organism="Streptomyces viridosporus"
Strein="A.914"
db_xref="texon:67581"
  Arisawa, A.
Diroct Submission
Submitted (07-OCT-1997) Akira
Marcian Corporation, 4-9-1 Joh
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Best Local Similarity 54.5%;
Matches 583; Conservative (
                                                                                                     Japan (E-mail:arise
Fax:81-466-35-1530)
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v.A4.29230 3030 bp mRNA linear PLN 03-JUN-2002
VOLVOX Carteri f. hagarlensis mRNA for pherophorin-dzi protein.
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Volvox carteri f. nagariensis.
Volvox carteri f. ragariensis
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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Glycoproteins during Extracellular Matrix Assembly in Volvox a
Plant Cell 14 (5), 1147-1160 (2002)
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                                                                                   Joynes 1 to 3030)
Wenzl,S.
Direct Submission
Submitted (30.JAN-2002) Wenzl S., Biochemistry I, University of
Submitted (30.JAN-2002) Universitaetsstr. 31, D-93053, GERMANY
Regensburg, Regensburg, Universitaetsstr. 31, D-93053, GERMANY
Location/Qualifiers
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9.7%; Score 191.2; DB 8; Length 3030;
Best Local Similarity 48.3%; Pred. No. 3.9e-15;
Matches 535; Conservative 0; Mismatches 573; Indels 0;
                                                                                                                                                                /organism="Volvox carter1 f. nagariensis"
/db_xref="taxon:3068"
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/function="structure"
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/protein_id="Cab22154.1"
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Arisawa,A., Matsutuji,M., Tsuruta,T., Dobashi,K., Makashima,T., Isshiki,K. and Yoshioka,A. To and Yoshioka and Yoshioka at Gene encoding a protect having asymmetric hydrolase activity for 4-substituted 1.4 Addingtopyridine derivatives and its expression
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                                   CCCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAAACGTCTACAAGGCCAT
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  Length 2539
Score 190; DB 6; Length 25:
Pred. No. 5.7e-15;
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RVTLITGDRALDAKGRYDGLDPAEKREHIPOQIRRSCHTLVVPADARAKLVSGKLD
GRLEDYTELMAATRHRGGLYTYGY RGARAARADVRDGTVRPADARLYCUSGKLD
GRLEDYTELMAATHRBOLKVYTYGY RGARAARADVRDGTVRAWEAGYDGKGV
TPQEAGAELHGYTDLKGCYTASKWTSPAPTGDVYGHGTHARASIAAGTGAGKGTV
KIAVLDTGVADTHPDLKGCYTASKWTSPAPTGDVYGHGTHARASIAAGTGAGKGTVK
KYAPGAKILMGKYLDAGEGDDSGTLAGKWAAAQGADIYNNSLCGNDTPETDFLEAA
VDKLSAEKGILFAINAGNEGPOSIGSPGSADSALTVGAVDNCRIATGGTSAMTPHVAGAAALLKQOH
PEWKYAELNGTATASAKGKTYDFEGGSGRYQVDKAITGGTSANTPHVAGAAALLKQOH
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TADFRLGGRANDGTYSAYVATGAGGSRYQVDKAITGGTSANTYRVLLDSGKAPANY
WAYLSGLIGLGRORS AYVAATGAGGSYRTAAAVEREVESKYNTYRVLLDSGKAPANY
WAYLSGLIGLGKDRSRAYPEAGAGGSYVLDASVLUGADPETWRGADWLAQP
KLDVIRNITYYVDARKAKPYKVTYPGKAAARAGFASADYTIETNDSAVSYGWULENYSG
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QVGMGAAA:GKKGAVTAFGWLPGSSCASGFSQPGKLPSFRTLYLSTVNGVTWDLDFED
LGGVDNEGWPIYDAVYTIGVGKTYKACKTYKRTVNTAVFGPRLTSSYGVFRDGNSIYG
VIPLFRADENSAFATSSAYTTLYFNGKKVGSNDPLFGEEGFTVPSGDAVRLTTS
VKRSAKVAAASHGSSSAYTTLYSGEKQLPVSSAFFAAVTGLDSKVAAGKRATPPV
VVBGAAQĞMLKSLAYVSYNGGKTWKKTTVTKGKITVKNPAKGKAISFRAKITDKKG
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/note="molecular masses observed on SDS/PAGE: 45kDa and
40kDa"
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Submitted (122 FEB:1996) Selichi Taguchi, Science University of
Submitted (122 FEB:1996) Selichi Taguchi, Science University of
Tokyo, Dept.of Edologeal Science and Technology; 2641 Yamazaki,
Noda, Chiba 278-6510, Japan (E-mail:staguchi@rs.noda.sut.ac.jp,
Tel:0471-24-1501(ax.448), Fax:0471-25-1841)
Sequence Underted (07-Nov-1996) by : Selichi Taguchi.
                                                                                                                                                                                                                                                                                                            subtilisin-like protesse.
Streptomyces albogriseolus (strain:S-3253) DNA, clone:SAM-P45.
Streptomyces albogriseolus
Bacteria: Actinobacteria: Actinobacteridae; Actinomycetales;
Streptomycinese; Streptomycetacesc; Streptomyces
                                                                                                                                                             083672
Streptomyces albogriseolus DNA for subtilisin-like protesse,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel member of the subtilisin-like protease family from
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Suzuki,M., Taguchi,S., Yamada,S., Kojima,S., Miura,K.I.
1337 CCGGCTCCGTCGCCGACAAGGGAAGCGCCACCCACCCTTCGACGTCAGC 1386
                            1857 TGAGCTTCGGCGTCCAGCASTGGCCGCACCACCGACGACGACGGCGGTCACC 1906
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/organism-"Streptomyces albogriseolus"
/atrain-"S 3253"
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/protein_id-*BAA12040.1*
/db_xref-*Gi:1694627*
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J. Bacteriol. 1798(2), 430-438 (1997)
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/clone="SAM-P45"
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/transl_table=11
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Bao,O., Tian,Y., Li,W., Xu,Z., Xuan,Z., Hu,S., Dong,W., Yang,J. Chen,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y., Ling, Tan,H., Chen,R., Wang,J., Yu,J. and Yang,H. Gonplete Sequence of the T. tengcongensis Genome Genome Res. 12 (\frac{\pi}{2}), 689-700 (2002)

Thermoanaerobactaritengcongensis.
Thermoanaerobacteritengcongensis
Bacteria: Firmicutes: Clostridia: Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.

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(bases 1 to 14376)

E 2 (bases 1 to 14376)

Baojo, Xu,Z., Ilu,S., Dong,W., Chen,Y., Wang,J., Yu,J. and Yang,H.

Blorect Submission

(I Submitted (07-0cr-2001) Beijing Genemics Institute/Genomics and
Bloinformatics Center, Institute of Genelics and Development,
Chinese Academy of Sciences, Beijing Airport Industrial Zone B6,
Delijing 101900, chid

E 3 (bases 1 to 14376)

Li,W., Xuan,Z., Yang,J., Ling,L. and Chen,R.

Sciences, Beijing 100101, China

Sciences, Beijing 100101, China

H (bases 1 to 14376)
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AE013049 AE008651
AE013049.1 GI:20515814
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     Length 3348;
     Score 182.4; DB 1;
Pred. No. 4.8e-14;
0; Mismatches 356;
           Query Match
Best Local Similarity 56.1%;
Matches 505; Conservative
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Tien.Y. Xue.Y., Xue,Y., Lai,X., Huang,L., Dong,X., Ma,Y. and Tan,H. Direct Submission
Submitted (0.00ct-2001) Institute of Microbiology, Chinese Academy of Sciences, Beljing 100080, China

1. 14376 /organism="Thermoanaerobacter tengcongensis" /strain="MB47"

/db_xref="taxon:119072"

265. .2374 /gene="GloA" /note="TTE0821"

278. .2374 265. .269 /gene="Glr

....--.mest Blastp hit - gi[2895904|gb|AAC01061.1| AF046916; glutamine synthetase type III [Ruminococcus 'lavefaciens], score 851, E-value 0"

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NGYSEGWYKEAEKRGLENIRSTVEAIPALIKEKNYKLMEKHGYLSKRELESRYEVLLE
NYIKTINI TALIMLDIAKROILPAVNKATKIAESINSYRATGLNVDISAOTELLAEV
SSLASEEKKHISELENAVNEASNANSDSYSKACYYRDYVFTKAGILREIGDKLETIVD
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GEOLFDILEQIENGGATTSKVGGVLKVGVSTLPALPKDSTDRNRTSPFAFTGNKFFER
WVGSSSSIAIATFILNTIVAESLSEIADRLEKASDFNEEVQLLLQEIVKHKRIIFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfan match to entry gln-synt, Glutamine synthetase, score 35.5; E-value 8:90E-11" complement(1255. 2681)
/note="TLR027, identity:88%, copy 9"
/product=fGlutamine synthase"
/protein=fG="AAM24078.1"
/db_xref=gD1:015015015
/translit_for="MOHILSEIFGSNVFNDSVMRERLFKATYKALRKTIDEGIPLEFA
/translit_for="MOHILSEIFGSNVFNDSVMRERLFKATYKALRKTIDEGIPLEFA
/translit_for="MOHILSEIFGSNVFNDSVMRERLFKATYKALRKTIDEFSGKELI
KGEPDASSFPSGGLRTTFFANKPOPLTGITARKRNSFISPTODGKVITEFSGKELI
KGEPDASSFPSGGLRTTFFANKPAMPCTSPAFIMDNTLXIPTAFCSYTGFALDLKIP
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FGARSPKGQEMEDHYFASIKERISAFWKDLDEELMKLGVPAKTKHNEVAPGQYELATV
YNTANTASDHGOLTMELMKKVALRHGLVCLLHEKPFAGINGSGKHINMSMSTDDGQNL
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/note-'putative rho-independent transcription terminator' complement (7778. 3360)
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/gene="GLaA"
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ACCESSION VERSION KEYWORDS

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/023 8339
/gane=*Papta*
/note="Best Blastp hit = gill26223|sp|P23914|LEVR_BACSU
TRANSCRIPTIONAL REGULATORY PROTEIN LEVR
91|98:39|ptr||A39160 transcription activator of levanase
operodilevR = Bacillus subtilis gill43150|gb|AAA22572.1|
(M60105) levR [Bacillus subtilis]
121086261|cmb|cAA6460.1| (%92868) transcriptional
regulaccry protein [Bacillus subtilis]
91|2655154|emb|CAB14650.1| (%92911) transcriptional
regulaccr (MIRANHLTC family) [Bacillus subtilis], score
291, E-value 2.00E-77*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILFIDEVHRIPPEGGENLFYLIDKGMYRRIGDFERKVNWIIJAAFTEKIDSILLRTF
IRRIFYLIQISPOERPVEKMEI VYLLRESKRIGVOLIISSHLGALISLEKYYEGN
IGEKSLIQISCERAFLANFOIRRFTKLDSALLPSKYKKEIINFFFDEFFIITPP
GKRSIDRYD; FEFIAGKYHELKSKGYEEKTIRDKIIDYVSNFLDDV*
                                                                                                            NIDVPNHYYISGYLPGSRYSOTWTFNATNTSYPIAITLIIPDMANYNPDFDIYLYDPS
GTLIKSSTGYGROEPTITLESOTGTYKVKYSYRGSGNYFPDLSAGGSEPVKY*
COMPLEMENT (3756. .6192)
/Gene**AprE2*
//note**Pfam match to entry Peptidase_S8, Subtilase family,
score 212;5, B-value 5,90E-60*
                                LGTSTSDGTDSTSLAVNRAVDSGTVVVVARGNSPAKYTIGSPGAREKALTVAMAD
VGELGFILLASFSSRGPTADGRIKPDTAARANSVIGYVTYSGTSMAPPVA
GTVALMLAANPIUTPDDAKTIMSTAKSWGPPSKNDVGAKRLDGYBAIRVAGNFRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry sigma54, Sigma-54 interaction domain, score 77.4, E-value 1.50E-20* complement(8414, .8657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_toble=11
/product="ntrC family Transcriptional regulator, ATPase
domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGTCGATACGGGTAT%GACG;GAACCACCCCGATCT---GAAGGGCAAGGTCATAGGCT
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                                                                                                                                                                                                                                                                                                  7455. 7814
/gene="PspF4"
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Matches 394;
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/transl_table_11
/product=Pytidoxine biosynthesis enzyme"
/product=Pytidoxine biosynthesis enzyme"
/product=Pytidoxine biosynthesis enzyme"
/db_xsef=G1:20515817
/db_xsef=G1:2051
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ypslpokiswqdsnknkifddleqrllnkpdseefpviitfnkpvsdädiffläknig
kfnikhrykiipsiaanlitksqinvlskleivkqieydepvyatldtatkffrar
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AGTGAGNSFYKGVAPDALLVGIKVLDANGSGSNSTVTAGIDWAVQNKDVYGIKVINLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Best Blastp hit = glill76057|spiP45293|xG47_HAEIN HYPOTHETICAL PROTEIN HI1647 glil074877|pir||F64173 hypothetical protein Hi1647 - Haemophilus influenzae (strain RW W20) g1157495|gb|haAc23294.1| (032837) conserved hypothetical protein (Haemophilus influenzae Rd), score 392, E-value 1,00E-108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote-"Pfam match to entry SOR_SNZ, SOR/SNZ family score 440.2, E-value 1.80E-128" complement(4235, 4239) /gene="Snzi" snzi" complement(4996, .6698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="mest Blastp hit = g1/7475581|pir||A69587|77|20
intracellular alkaline serine proteinase aprx - Bacillus
subtilis g1|2534110|emb|CAB13610.i| (299113) alkaline
serine protease [Bacillus subtilis], score 210, E-Value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
/product=2subtilisin-like serine proteases"
/protein_1d="AAM24081.1"
/db_xref="GI:20515818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4996. .6681)
/gene="AprE2"
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/gene-"Snzl"
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/note="TTE0824"
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SCC24
Streptcomyces coelicolor cosmid C24.

ALISTODA ALG45882
ALISTODA ALG45882
ALISTODA ALG45882
ALISTODA GG CARLOVALURE: Alpha-L-arabinofuranosidase;
calcium-binding protein; carrier protein; fatty acid synthase;
calcium-binding protein carrier protein; fatty acid synthase;
calcium-binding protein carrier protein; fatty acid synthase;
protein; protein kinase; carrier protein; spermidine, sprinting protein; sugar kinase; sugar transporter inner membrane
protein; sugar transporter sugar binding protein; transcriptional
regulator; two-component sensor histidine kinase.
Streptomyces coelicolor A3(2).
Actinomycetales; Streptomycineae; Streptomycetaceae: Streptomyces.

L (Abase I to 4089)
Actinomycetales; Streptomycineae; Streptomycetaceae: Streptomyces.

Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physicai map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome

M. Mirrobiol. 21 (1), 77-96 (1996)
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Direct Submission
Submitted (03-APR-2000) Streptomyces coellcolor sequencing project, Sanger Centre, Wellcoome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                  5681 ATGTAGGTGAACTTGGCTTTAACCTTGCAAGCTTTTCCAGCGGGGGGGTCCTACTGCTGACG 5622
                                                                                                                                                                                                                       911 CCTACACCGTCGCCTCACCCGCCGCCGCGAGCAAGGTCATAACCGTC------G 958
671 GCGCGAAGCTCGTCGGCGTCAAGGTTCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCA 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTACGGGATAAGGGTCATCA
                                                                                                                                                                                                                                                                                                                                    851 ACAACGCCTGGGACGCCGGTATAGTAGTGGTCTGCGTCGCCGCCGCCAACAGCGGCGGCCGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGCCTCAAGCCGGAAGTCGTCGCCCCGGCGTTGACATCATAGCCCC 1067
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Brown, S.P. and Harris, D.
Unpublished
3 (bases 1 to 40899)
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SCC24/c
LOCUS
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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in codons is given for each CDS.

In codons is given for each CDS.

Usually the highest scoring match found by fasta to is given for cost of solutions. The truth cost of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Generally developed gidden warkov wodel (Krogh et al., Nucleic Acids Research, 24(23):4768-4778[1944]) and the Frameslot program of Bubb et al., Gene al., 188-4778[1944]) and the Frameslot program of Bubb et al., Gene al., 187-56(1984) as implemented at http://www.nlh.go.jp/
jun/ogi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If may be shorter because we arrange for a sequenced clone. It may be shorter because we arrange for a small overlap between and overlaps with cosmids C42 and 7A8 on the Asel-C genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2770. .3633)
/gene="SCC24.03c" possible sugar transporter membrane protes. SCC24.03c" possible sugar transporter membrane protes. In the service se
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/db_xrefatton:100226*
/clone='qosnid C24*
/clone='qosnid C24*
/clone='fosnid C24*
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/gene="SCC2431; abfA"
/complement(1237.2742)
/gene="SCC24.02c"
/note='SCC24.02c'
/note-'SCC24.02c'
/n
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/translelloloson
Atenana Lalen-"MRTAILDPREYORAVNPRIFOSFVEHLGRCVYTGVFEDGHPT
ADABOLRODVLEHVRELOVYRTGGGHPYGGY KREDSVGPYEDRERALDLARRSTET
NRFGLSEYIALKKIGPQAEPMAAVNLGTRGVABALELOSVANHPSGTALSDLRAEHG
DDDPROT RIAMCLGNREMOFMYOFMYRAEVGRAAFTARRRQIDDPDELVAGGSSGG
SMETPRAEMRAYVLKETYDLYDNISLIRAYYEPHDGDVDSFLASAVUMESTIENYATCB
HVGARLKSKKX YILSFDEMNYMTMITKTOAEVSALDWPEAPRILEDNYSYMDAYYFGSL
LIALLRAINDRYTYAKLGAOLVNY TAFNTEGGSTRRQIPPROTSTENYSYRGKEYLDYR
VDSFTYDTAXYGRADLLAALAYRAEGGSYYVEAVNRSRTGALPLESALSGLELTEVVE
HSALADADDDARRYTLAEPERVYPHPYDGTSLRDGRLTAALEPLSWNSIRLR
numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                        The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organisms Streptomyces coelicolor A3(2)"
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/protein_id="CAB86096.1"
/db_xref="GI:7414545"
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/gene="SCALA; 03c"
/note="SCO2432"
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complement(1830. .4571)
/gene="SCC24.04c"
/gene="SCC24.04c"
/note="SCC24.04c"
/note="SC24.04c"
/note="SCC24.04c"
/note="
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/product="putative sugar transporter membrane protein"
/product="putative sugar transporter membrane protein"
/protein_id="cab86098.1"
/db_xref="g=17414547"
/d
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//gene="SCC24 05c"
//gene="
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Binding-protein-dependent transport systems inner membrane
component, score 81.20, E-value 2.2e-20,
component(3071. .3123)
/gene="SSC24.03c"
/note-"PS00402 Binding-protein-dependent transport systems
inner membrane comp sign."
/gene="SSC24.04c"
/gene="SSC24.04c"
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SYROGYSALSITEPVLLAAVALARMWLLRNREEGGF"
Complement(3641...3647)
/gene="SCC24.04c"
/gene="SCC24.04c"
/product="putative sugar transporter membrane procession to the control of the co
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Binding-protein-dependent transport systems inner membrane
component, score 39.00, E-value 1.1e-07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-*PS00402 Binding-protein-dependent transport systems inner membrane comp sign." complement(4568. :5926) /gene-*SCC24.05c*
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/gene="SCC24.03c"
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/gene="SCC24.04r
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/translation-"MGRPGLNRRHFCAAAGGLTVAGSFGFAALGTGADALASGADTRV
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YMHLGRVTGFSPGFLLDFPWDPALLARYGYREODFRPELMKRAVIDGKLVALPLOIHVO
LCFYRKDVLKRAGLLGEDGRIVPVESTEEWFDVLKEARKATAKGLOTIGLWHNDONFO
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                                                                                                                                                                                                                                                                                                                                                            471 CGCAAGCGGTGTGGTTGCCATCGTCGATACGGGTATAGACGCGAACCACCCGGATCT 530
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                    /product putative sugar transporter sugar binding
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                                                                                                                                                                                                                                                                                Length 40899,
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                              Score 170.8; DB 1;
Pred. No. 7.7e-13;
0; Mismatches 602;
                                                                                                                          /protein_id="CAB86099.1"
/db_xref="G1:7414548"
/db_xref="SPTREMBL:09L0B2"
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Amino acid transport integral membran protein; branched amino acid
binding secreted protein; branched amino acid transport system

ATP-binding protein; branched amino acid transport system permease;
integral membrane protein; ion transport integral membrane protein;
polysaccharide blosynthesis protein; regulator; regulator; protein;
secreted amidase; secreted peptidase; secreted protein;
secreted regulator; transcriptional regulator;
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Submitted (03-AdG-2000) Streptomyces coelicolor sequencing project,
Submitted (03-AdG-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Profe
David A Hopwood, [3] John Innes Centre, Norwich Research Park
Colney, Norwich, Norfolk NR4 7UH, UK
On May 9, 2002 this sequence version replaced 91:9716211.
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Redenbach.M. Kleser.H.W. Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
MOI. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                        1359 AAGGGCCACCACACCTTCGACGTCAGGGGGCCACCTTCGTGACCGCCACCTCTACT 1417
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                                                       20740 carcaccecaccescacceccaccresscrrcracresscrasscassccacca 20681
                                                                                                                                                                                                                                                                                                                   20440 cecertegreaagaegeceaecegracacecreacegrecacereaagaececrecegrap391
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1299 GGCCATCAAGTACGACGACTACGCCAAGCTCACCTTCACCGGCTCCGTCGCCGACAAGGG 1358
                                                                                                                                                                                                                                                     1418 ------GGGACACGGGCTCGAGCGACATCGACCTCTACCTCTACGACCCCAACGGGAA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1530 GACCGCCGGAACCTGGACGGTCAAGGTCGTCAGCTACAAGGGCGCGGGGGAACTACCAGGT 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1590 CGACGTCGTCAGCGACGGGAGCCTCAGCCAGTCCGGCGGCGACCCGAACCGAATCCAAACCC 11649
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                                                                                                                                                               20680 GCCGGTCACCAGGACCGTCGCTCACACTCCTCGGACACGGACGTGAAGCŢ
                                                                                                                                                                                                                                                                                                                                                                                     1470 CGAGGTTGACTCCTACACCGCCTACTACGGCTTCGAGAGGTCGGCTACTACAACCC
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Streptomyces coelicolor A3(2)
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
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Streptomyces coelicolor sequencing at The Sanger Centre is

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controlly. The cosmit name, or (itsel tob), c (comprementary strand).

The more significative matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasts -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribbsome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(23) 4768 4778 (1994) and the Frameplot program of subb et al., Gene 30:157-468 4778 (1994) and the Frameplot program of subb et al., Gene 30:157-66 (1984) as implemented at http://www.nih.go.pp.

Jun/C91-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (adg. ggv, ttg. or (att)) which is preceded by an upstream initiation codon.

Inbograme initiation codon. This cannot be identified we choose the most upstream initiation codon.

Inbogram: This sequence (att) why Nor be the entire insert of the sequenced clone of the sequence coverlapping sections once, or longer, because we arrange for a small overlap between enterpring submissions. Cosmid 8A11.
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/gene="5C8411.03*
/note="5C8411.03, possible regulator, len: 156 aa; similar
to TR:0952F (EMBL:AL096852) Streptomyces coelicolor
putative regulator SCE19A.24, 142 aa; fasta scores: opt:
272 z-scoze: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="nominal overlap with Streptomyces coelicolor cosmid
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ftvtydgyraevaglmgatebeftrprssagrlrarpaprracrgw"
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/note-"PS00622 Bacterial regulatory proteins, luxR family signature"
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL: http://www.sanger.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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/note="Pfām match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 49.10, E-value
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/protein_jc.*CaC01574.1*
/db_xref="GR:9716213"
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/gene="SC3A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
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/transl_table=11
/product**putative regulator*
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/gene="SC8A11.02c"
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/gene="SCEA11.03"
/note="SCC7175"
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//note=*SC8A11.04c.
//note=*
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AATVGAWNDFGKGVDDADFSSRGPRVGDLAWFRDLTARGVGVLAAKSRYAPEGEGAY
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OSLGGTSMATPHVAPGALLAAEHPDHTGORLKEALVGTATGORFSFFDAGSGRVUD
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RATLALTARDHHDKPLSGTVILKDRVERNTAFVSVDAGSGLDLRLSFGTTSVGVNKEGR
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YTGSRSPQLBGTRATRWWAGGGARFERGEVRRVARTRSOLOPPLTSGGGGTFDD
YTGSRSPQLBGTRATRWWAGGGARFERGEVRRVARTRSOLOPPLTTSGGGTFDD
RAGRICLLLUNGTGKPPWADLPBAAPLFVASLGTDDSRALLARFRGGFTFLRVV
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RAGRECLLLUNGTGKPPWADLPBAAPLFVASLGTDDSRALLARFRGGTFTLLVV
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IOHPRILSDNGTSGOGPFRAGONISTSWATAMGDSGGHAGVVWADCDTRISLYOGGE
LIGEDVWRNIWWYGGLSPGPK PYFULEGSRNLPDRPYSTRTWADFSATTDPTRL
TPLPLVQLDYAVROLSGRAHRRIELTWTASHLEGAAGAAIRTHVEVSYDDGATWH
RTALRKSADGWTARLDAPGRARVASLRTTAKDTEGNGVGGTLIRAFGLR
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PDHFLLVYIRFAEGAPPYWHYGROLLHEGLRTTSGLGDVQVAADTPDRFTAALQV
NAHGDIAIFSLEVPELEEWIDRYYLHVPAGTESSRLGTDAFLSKLFDEPEÄSSR"
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rnote-'Pfam match to entry PF02225 PA, PA domain, acore 19.00, E-value 0.058"
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htstidine active site"
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/note="De-
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/gene="SCBAll.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 CATACAGGAGGATTACAAGGTTCAGGTTGACGACGCCACTTCCGTCTCCCAGATAGGGGC 440
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/gene="SCBA11.04c"
/note="PSOA13.04c"
sopertic acid active afte"
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50.9%; Pred. No. 4.3e-10;
tive (0; Mismatchee 475; Indels 33;
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7295. 7739

7295. 7939

7906-*SC8A11.05*

/codon_start=1

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Best Local Similarity 50.99
Matches 527; Conservative
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20842 dececcedecadereacededececedrecedecerecresranceracadadadacadecede 20783
                                                                                                                                                                                                      20902 CGGCCGGGTGGACGTCGACGCGGGGGGCGCGCGGGTGTACGCCTCGGCGACGCCCAA 20843
                                 21016 GGCGGCGCTCTGCTCGCCCGCCGCACCTCCTAGCGCCAGCGCCCCTCAAGAAGACGTEZQ95%
                                                                                                                                                                                                                                                        1338 CGGCTCCGTCGCCGACAAGGGAAGCGCCACCACCTTCGACGTCAGCGGCGCCCACCTT 1397
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                                                                                     1218 CCTCATCGAGACCGCCGACATAGTCGCCCCCAAGGAGATAGCGGACATCGCCTACGGTGG"1277
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Search completed: November 2, 2002, 10:23:32 Job time : 3523.5 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

November 2, 2002, 08:16:03; search time 51.5 Seconds (without alignments) (without alignments) 11772.815 Million cell updates/sec Run on:

US-09-841-553-2 1977 1 ATGAAGAGTIAGGTCCTGT......AGGCCGTCGTCTACTACGGG 1977 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 441362 seqs, 153338381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*

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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STAMMENTES

	Description	Sequence 2, Appl1	Sequence 11 Appl	Sequence 6, Appl 1	Sequence 15 . Appl	Sequence 7 Appli	Sequence 17, Appl	Sequence 34, Appl	Sequence 15 Appl	Sequence 4 SAppl 1	Sequence 2; Appl1	Sequence III sppl	Sequence 14 Appl	Sequence 1, Appl1	Sequence 1, Appl1.	Sequence 37 App11		Sequence 26, Appl		2	2	~	÷	V	Ö	'n	4	7
SUMMARIES	QI	US-08-894-818B-2	US-09-445-472-11	US-08-894-818B-6	-08-894-	US-08-750-532-7	80-	-08-83	9	-08-83	ė	B			6	05-09-000-016-3	US-09-514-340-3	US-08-894-818B-26	US-09-023-173-4	US-08-750-532-10	US-08-894-818B-13	4 US-09-103-840A-2	US-08-700-651-1	18-928-3	-200-65	뽄	US-09-025-691-4	US-08-928-361B-2
	Length DB	1977 4	1977	1977 4	1859 4	868	1464 4	1962 4	1962 4	1566 4	1236 . 4	564 1	564 4	2809 3	2809 4	2539 3	2539 4	507 4	1140 3	145 1	145 4	4403765	5163 3	5163 3	5318 3	5318 3	2712 3	5511 3
ď	Query Match	100.0	100.0	68.8	58.9	42.1	40.8	37.9	37.9	35.0	28.3	56.9	86.9	9.7	7.6	9.6	9.6	7.4	6.3	e. 9	6.3	5.7	5.4	5.4	υ. 4	₽.	ω. 	4.9
	Score	1977	1977	1360.8	1165	833.2	806.8	750.2	750.2	692.8	560.4	532.8	532.8	191.6	191.6	190	190	145.4	125.4	124	124	113.2	107.6	107.6	107.6	107.6	104.2	97.4
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Sequence 1,	Sequence 1,	Sequence 7,	Sequence 5,	Sequence 2,	Sedneuce 3,	Sednence 35	Sednence 35	Sednence 35	Sequence 35	Sednence 35	Sequence 3:	Sequence 3:	~	Sednence 36	ď	Sednence 26	Sednence 36	
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	Sequence 2, Application US/08894818B	MATTON	TAKAKURA, HIKaru	MORISHITA, MIO	MITTA MASSOCI	ASADA, K1yozo	TSUNASAWA, Susumu	NATO, IKUNOSAIN VENTION: HYPERTHERMOSTABLE PROTEASE GENES	••	U)	Browdy and Neimark	nth Street N.W., Ste.	TO SUTURPE	United States of America	04	COMPUTER READABLE FORM:	PE: Floppy disk	COMPUTER: IBM PC compatible		COLIMAND: FOLDMILL MOLDBOOK *1.0, VOLULOI	APPLICATION NUMBER: US/(8/894,818B	-MAY	ATION: 435	PRIOR APPLICATION DATA:	APPLICATION NUMBER: PGT/JP96/03253 PILING DATE: 07-NOV-1498	PRIOR APPLICATION DATA:	APPLICATION NUMBER: JP 323285/1995		Browdy, Roger	·	REFERENCE/DOCKET NUMBER: TAKAKURA=1	TELECOMMUNICATION INFORMATION:	- 1	INFORMATION FOR SEC ID NO: 2:	SEQUENCE CHARACTERISTICS.	1977 base patter		23		TTUGGE
RESULT 1	Sequence 2,	: Patent No. 6261822 ; GENERAL INFORMATION:	APPLICANT:	APPLICANT	APPLICANT	APPLICANT	APPLICANT	TITLE OF INVENTION:	NUMBER OF SEQUENCES	CORRESPONDE	; ADDRESSEE:	2	CTITO .	ີ:	0	; COMPUTER RE	. MEDIUM TY	COMPUTER:	COPERATING	CIRRENT ADD	APPLICATI	: FILING DATE:	: CLASSIFICATION:	PRIOR APPLI	, APPLICATION :	, PRIOR APPLI	; APPLICATI	PILING DATE:	NAME: Br	REGISTRAT	REFERENCE	TELECOMMUNI	TELEFRONE:	INFORMATION F	, SEQUENCE CH	; LENGTH:	TYPE: nu	STRANDEDNESS:	. 200 1000	

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Sequence 117 Application 09/09445472 Seq 10 NV: 11 X MOT patent No. 635940 Seq 10 NV: 11 X MOT patent No. 635940 Seq 10 NV: 11 X MOT patent No. 635940 Sex Seq 10 NV: 11 X MOT patent INFORMATION: 0.0 NV MOT MARKURA, Hikaru
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APPLICANT: SHIMOJO, TOMOKO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: KATO, ILUNOSDIN
TITLE OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAUGRA-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
FRICH FILING DATE: 1997-16-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PETCENTIN VETSION 3.0
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2y 162	21 TCGGGGGGGGGAACCCGAATCCAAACCCGAACCCGAACCCGAACCCGACCGGACCGACC	980
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Ob 174	41 GTCAACAGCGGTGCCACCAAGATAACCGGTGACCTGGACTTCGATACTTCCTACAACGAC 180	300
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                  170 ACCAGGAAGIGGACACCGICAIAAIGIICGGGAGCIACGGAACAGGGACAGGGCGGITA 229
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                                                                            1921 GCCTACACACCTACGCTGGGCGGACTACCAGCTCCAAGGCCGTCGTCTACTACTACGGG 1977
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Pred. No. 2.2e-263;
0; Mismatches 292; Indels 9;
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: INP PC compatible
COMPUTER: INP PC compatible
CONFINER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                            419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAKAKURA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                         APPLICANT: TAKAKURA, n.m...
APPLICANT: MORISHITA, Mio
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MITTA, Maganori
noridant: MITTA, Maganori
ASADA, Kiyozo
                                                                                                                                                                       Sequence 6, Application US/08894818B
Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                             Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Browdy, Roger L,
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owery Match
Best Local Similarity 83.9%;
Matches 1573; Conservative
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SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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11: Washington
STATE: D.C.
COUNTRY: "-
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230 AGGYACTGAGGCTCATGGGGGGCCCAGGTCAAGTACTCCTACAAGATAATCCCTGCTGTCG
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                                   GGTCCACGTCGAGGAACAGCTACGAGGTCGAGTACGCCAACCCCGGCCCGGGAACCT 1903
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                                                                                                            CCTACACCGCCTACTACGGCTTCGAGAAGGTCGGCTACTACAACCCGACCGCGGGAACCT 1543
                                                                                                                                                GCACGGTCAAGGTCGTCAGCTACAAGGGCGCGGGGAACTACCAGGTCGACGTCGTCATAGCG 1603
                                                                                                                                                                                    ACGGGAGCCTCAGCCAGTCCGGCGGCGGCAACCCGAATCCAAACCCCAACCCGAACCCAA 1663
                                                                                                                                                                                                                                                            ACACCTTCACCATGAACGTCAACAGCGGTGCCAACAAAAACCGGTGACCTGACCTTCG 1783
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US-08-894-818B-15
US-08-894-818B-15
Sequence 15. Application US/08894818B
Patent No. 6261822
GENERAL INFORMATION:
APPLICANT: TAKAKUGA, Hikaru
APPLICANT: TAKAKUGA, Hikaru
APPLICANT: MITTA, MABANOTO, KATBUİKO
APPLICANT: ASADA, KİYOZO
APPLICANT: KATO, Ikunoshin
TILE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 4
STORESPONDENCE ADDRESS:
ADDRESSEE: Broudy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United ct.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                           TCGTCTACTACGGG 1977
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CAAGGGAAGCGCCACCCACACCTTCGACGTCAGCGGCGCCCACCTTCGTGACCGCCACCCT 1412
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58.94; Score 1165; DB 4; Length 1
Best Local Similarity 100.04; Pred. No. 2.8e-224;
Matches 1165; Conservative 0; Mismatches 0; Indels
                       Patentin Release #1.0, Version #1.30
OPERATING SYSTEM: FC-POS/MS-DOS
SOFTWARE: PAtentin Release 11.0, Versic CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818D
FILING DATE: 20-MAY-1998
CLASSIFICATION A45
PRIOR APPLICATION BATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: UP 521285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BTOWdy, ROGEL LORSERFATION NUMBER: 25,618
REGISTATION NUMBER: AMARKURA-1
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                TELEPHONE: (202) 628-5197
TELEPHONE: (202) 628-5197
TELEPRATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                        : TOPOLOGY: linear
MOLECULE TYPE: genomic DAR-
US-08-894-818B-15
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661 GGTTGACTACTCCTACACCGCCTACTACGGCTTCGAGAAGGTCGGCTACTACAACCCGAC
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COUNTRY: D.C.
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: C
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APPLICANT: MANAWOTO, Katsuhiko
APPLICANT: MANAWOTO, Katsuhiko
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TSUNASAWA, 14PERTHERMOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: BROWDY AND NEIMARK, P.L.L.C. 419 Seventh Street N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILLIA DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1141 GCTCAAGGCCGTCGTCTACTACGGG 1165
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Patent No. 5756339
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1006 CCGACCGCGGACGGAAGCCTCGAAGCCGGACGCCCCCCGGCGTTGACATCATAGCC 1065
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42.14; Score 833.2; DB 1;
Bost Local Similarity 97.04; Pred. No. 4.4e-158;
Matches 874; Conservative 0; Mismatches 24;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/173912,
PILING DATE: 26-7UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (202) 628-5
                                                                                                                                 REFERENCE/DOCKET NUMBER
                                                                                                                                                                    TELEPHONE: (202) 628-552
TELEFAX: (202) 737-552
INFORMATION FOR SEQ ID NC: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  LENGTH: 898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     / TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
US-08-750-532-7
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                                                                                                                                                                                                                                     Length 1464:
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: TAKANURA, HIKATU
APPLICANT: TAKANURA, HIKATU
APPLICANT: MANANOTO, Katsuhiko
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, KILOZO
APPLICANT: ASADA, KILOZO
APPLICANT: SADA, KILOZO
APPLICANT: KATO, IKUNOSHIN
TITLE OF INVENTION: HYPERTHERNOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

REDIGH TYPE: ELOOPY disk
COMPUTER: ELOOPY disk
COMPUTER: IBM PC COMPALIAL
COMPUTER: IBM PC COMPALIAL
COMPUTER: IBM PC COMPALIAL
COMPUTER: IBM PC COMPALIAL
SVETHARE: PACENIAL Release #1.0, Version #1.30
SOFTWARE: PACENIAL Release #1.0, Version #1.30
SOFTWARE: 20-MAY-1998
CLASSIFICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 12-DEC-1995
FILING DATE: 12-DEC-1995
FILING DATE: ROADAY ROADER TO FORMATION:
NAME: ROADAY ROADER TO FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 806.8; DB 4;
Pred. No. 8.9e-153;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                              E: Browdy and Neimark
419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., S
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
                                                                                                                                                                                                                                                   Sequence 17, Application US/08894818B Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 25.618
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: TAKAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ. ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.1%;
Matches 811; Conservative
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STRANDEDNESS: double
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US-08-894-818B-17
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1127 GTGGTGGTTGCCATGGTGGATACGGGTATAGACGCGAACCACCCCGATCTGAAGGGCAAG 1186
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301 AAGGCCAGGGACCTTCTCCTGATCGCGGGCATGATAGACACGGGTTACTTCGGTAACACA 360
                                                                       61 GCCCTTGCGGCACCCGTAAAACCGGTTGTCAGGAACAACGGGGGTTCAGCAGAAGAACTAC 120
                                                                                              GGACTGCTGACCCCGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGAACCAGGAAGTG 180
                                                                                                                                                                                                                              181 GACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGCGTTAAGGTACTGAGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/0894818B
Patent No. 2651822
GENERAL INFORMATION:
APPLICANT: TARAKURA, HIRERU
APPLICANT: WORISHITA, Mito
APPLICANT: WARAMOTO, Aatshiko
APPLICANT: MITTA, Masandri,
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susmu
APPLICANT: KATO, IKUNOSħio
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1112 ACACAGCAGCTCCTGGGA.ATCAATGGCAACTCCTCACGTAGCTGGTATTGCAGCCCTCT 1171
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                                                             GCAGCG---TTAACTCCCAGTACATAGGCGTCGCCCCCGGCGCGAAGCTCGTCGGCGTCA
                                                                                                                                                 AGGITTCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCATCATCGCGGGTGTTGACTGGG
                                                                                                                                                                           752 TOGTOCAGAACAAGACAAAGTAUGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTTAAAATAAAGGCCAGGGACCTTCTGCTGATCGCGGGCATGATAGACACGGGTTACT 349
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37.9%; Score 750.2; DB 4; Length 1962;
Best Local Similarity 64.7%; Pred. No. 1.9e-141;
Matches 1219; Conservative 0; Mismatches 618; Indels 48;
  419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                       TLLING DATE: JUTATIONS
CLASSIFICATION: 435
PRIOR APPLICATION NDTA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: JP 332285/1995
APPLICATION NUMBER: JP 332285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGET L.
RECISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAKAKURA-1
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1962 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                            CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
                                                               United States of America
                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
HOLECULE TYPE: genomic DNA
US-08-894-818B-34
                                                                                                         OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Bost Local Similarity 64.7%; Pred. No. 1.9e-141;
Matches 1219; Conservative 0; Mismatches 618; Indels 48; Gaps
CTCCACAACCAGAACCAACAGTAGACGCAAAGACGTTCCAAGGATCCGATCACTACTACT
                                                                                                                                                                                                                                                                           Sequence 15, Application US/09445472;
Sequence 15, Application US/09445472;
Patent No. 6358726;
CENERAL INPORMATION:
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, TOMOKO
APPLICANT: SHIMOJO, TOMOKO
APPLICANT: SHIMOJO, TOMOKO
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKHURA-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT APPLICATION NUMBER: US/09/197
PRIOR FILING DATE: 1999-10-10
NUMBER OF ESQ ID NOS: 33
SOFTWARE: PATENTI VEFSION 3.0
SEQ ID NO 15
LENGTH: 1962
                                                                                                                                                                                                                 1952 AGCTCAAGGCCGTCGTCTACTACGG 1976
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                                     395 CAGCAGAATTAGAAGGACTGGATGAGTCTGCAGCTCAAGTTATGGCAACTTACGTTTGGA 454
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                                                                           ACTCCCTCGGCTACGACGGAAGCGGTGTGGTTGCCATCGTCGTACGGGTATAGACG
                                                                                                              ACT...-TGGGATATGATGGTTCTGGAATCACAATAGGAATAATTGACACTGGAATTGACG
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1592 ACGICCICAGCGACGGGAGCCICAGCCAGTCCGGCGGCGGCGCAACCCGAATCCAAACCCCA 1651
                                                                                                                                            1637 CTCCACAACCAACACACACAGAAGACGCAAGAAGACGATCCAAGGATCCGATCACTACT 1696
                                                  CCGCCGGAACCTGGACGGTCAAGGTCGTCAGCTACAAGGGCGGGGGGAACTACCAGGTCG 1591
                                                                                                                                                                                                                                                            1712 GGGACACCAGGGACACCTICACCAIGAACGICAACAGGGGIGCCACCAAGAIAACCGGIG 1774
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                                                                                                                                                                                                                                                                              1652 ACCCGAACCCAACCCCGACCACCGACCAGACCTTCACCGGTTCCGTTAACGACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08894818B
Patent No. 6261822
GENERAL INFORMATION
APPLICANT: TARAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: MAMAMOTO, Katsuhiko
APPLICANT: MAMAMOTO, Katsuhiko
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO
ITILE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Nelmark
STRET: 419 Seventh Street N.W., SLe. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/894,818B
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1116 CAAGGCCTCTGGAACCAGCATGGCCACCGCACGTTTCGGGCGTTGGCGCTCATCCT 1175
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                                                                     TAKAKURA-1
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25518
'REFERENCE/DOCKET NUMBER: TAKAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-519'
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
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                                                                     GGGAAGCGCCCACCCCACCCTCGACGCGCGCCCACCTTCGTGACGCCCCCTTA 1415
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| Sequence 2, Application US/09445472
| Patent No. 6158726
| GENEBAL INFORMATION:
| APPLICANT: TAKANURA-
| APPLICANT: ASADA, Hikaru
| APPLICANT: ASADA, KLYOZO
| APPLICANT: ASADA, KLYOZO
| APPLICANT: ASADA, TKUNOSHIN
| TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE FILE REFERENCE: TAKANURA-6
| CURRENT PILLMG DATE: 1999-12-06
| PRIOR FILING DATE: 1997-06-10
| PRIOR FILING DATE: 1997-06-10
| NUMBER OF FOU IN UNBER: 151969/1997
| NUMBER OF FOU IN OSE 33
| SOFTWARE: PATENTIN VETSLON 3.0
| SEQIENT NO. 2
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CAAGGCCTCTGGAACCAGCATGCCCACCCGCACGTTCGGGGCGTTGGCGCGTCATCCT 1175
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                                                                                                                                               459 CCTCGGCTACGACGGAAGCGG\(GTGGTGGCTTGCCATCGTCGATACGGGTATAGACGCGAA 518
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                                                                                  Length 1236;
                                                                                                                  Indels
                                                                                  28.3%; Score 560.4; DB 4;
68.0%; Pred. No. 1.4e-103;
1ve. 0; Mismatches 371;
TYPE: DNA
ORGANISM: Artificial Seguence
                              ; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-445-472-2
                                                                                                  Best Local Similarity 68.09
Matches 796; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1116
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JS-08-750-532-1
022-273-5
C11-277-5
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                                                                                                                                                1476 TGACTACTCCTACACCGCCTACTACGCCTTCGAGAAGGTCGGCTACTACAACCCGACCGGTSTS
                                                            1416 CTGGGACACGGGCTCGAGCGACATCGACCTCTACGACCCCCAACGGGAACGAGGT 1475
                                                                                                                                                                                   1536 CGGAACCTGGACGGTCAAGGTCGTCAGCTACAAGGCCGCGGCGAACTACCAGGTCGACGT 1595
                                                                                                                                                                                                                                                                    APPLICANT: YAWAWOTO, KRISUNIKO
APPLICANT: MORISHITA, MIS
APPLICANT: ASDA, KIYOZO
APPLICANT: TSUNASAWA, SUSUMU
APPLICANT: TRATO, I KUROSHIN
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
ODPHYDER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTMAKE: PASTEM: PC-DOS/NS-DOS
SOFTMAKE: PASTEMIN DC-DOS/NS-DOS
APPLICATION NUMBER: US/08/750,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...OMESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                 1596 CGTCAGCGACGGGAGCCTCAGCCAGTCCGG 1625
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/UP95/01095
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/130236
FILING DATE: 11-JUN-1994
PRIOR APPLICATION NUMBER: JP 1994/173912
FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
RECISTRATION NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08750532
Patent No. 575639
GENERAL INFORMATION:
APPLICANT: MITTA, Masanori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1078 GGAACCAGCATGGGGACCCCGÄTAAACGACTACACCAAGGCCTCTGGAACCAGCATG 1137
                                                                                                                                                                               484 GGAACCAGCATGGGCACCCCGATAAACGACTACTACAACCAAGGCCTCTGGAACCTCAATG 543
                                                                                                                                                                                                                                                                                                                                                                                                                        364 GGIGCAGITGACAGCAACGACAACATCGCCAGCITCICCAGCAGGGGACCGACCGCGGAC 423
                                                                             598 CACGGAACCCACGTIGCGGGS%CGTIGCCGGAACCGGCAGCGTIAACICCCAGIACAIA 657
                                                                                                                                                           658 GGCGTCGCCCCCGCCGCGCAAGTCGTCGGCGTCAAGGTTCTCGGTGCCGACGGTTCGGGA 717
                                                                                                                                                                                                                                       718 AGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTACGGG 777
                                                                                                                                                                                                                                                            838 AGTCAGGCCGTCAACAACGCCT\GGACGCCGGTATAGTAGTCTGCGTCGCGCGCCGCAAC 897
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                                                                                                                  4 CACGGAACTCACGTGGGGGGAACAGTTGCCGGAACAGGCAGCGTTAACTCCCAGTACATA 63
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    Length
                                         17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC competition
COMPUTER: TRM PC competition
COPFRAING SYSTEM: PC-DCS/NS-DOS
COPFRAIR: Patentin Release #1.0, Version #1.30
26.9%; Score 532.8; DB 1; 97.0%; Pred. No. 3.9e-98; Live '0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Browdy and Welmark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNRY: United States of America
2.P: 2004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08894818B Patent No. 6261822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKAKURA, Hikaru
MORISHITA, Nito
YAMAMOTO, Karsuhiko
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APPLICANT: MITTA, Masancott
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Sukamu
APPLICANT: KATO, Ikunoshia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97:00
Matches 543; Conservative
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US-08-894-818B-14
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SHERAL INFORMATION:
APPLICANT: AKITA ARISNA et al.
APPLICANT: AKITA ARISNA et al.
APPLICANT: AKITA ARISNA et al.
APPLICANT: AKITA ARISNA et al.
TITLE OF INVENTION: GENÉ ENCODING A. PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HYDROLES ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE
TITLE OF INVENTION: ITS EXPRESSION PRODUCT
NUMBER OF SOUBNICES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, 41nd & Ponack, L.L.P.
STREET: 2033 K Street. N.M., #800
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                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: WASHINGTON
ZITE: D.C.
COUNTRY: U.S.A.
ZIPE: 2006
COMPUTER READABLE FORM:
MEDIOW TYPE: DISKETE, 3.5 inch, 1.44 mb
COMPOTER: IBM COMPETIBLE
OPERATING SYSTEM: MS-DCS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U3/09/00,016
FILING DATE: January 36, 1998
CLASSIFICATION NUMBER: 33,000,016
RELING DATE: THORNATION:
APPLICATION NUMBER:
RELING DATE:
RECISTRATION NUMBER: 33.367
REFERRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces viridosporus
STRAIN: A-914
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ORGANISM: Streptomyccs antibioticus
  1, Application US/09000016 6143541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2540...28C9
IDENTIFICATION METHOL:
US-09-000-016-1
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                                                                                                                                                                                                                                                  Washington
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LOCATION: 338.
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26.9%; Score 532.8; DB 4; Length !
Best Local Similarity 97.0%; Pred. No. 3.9e-98;
Matches 543; Conservative 0; Mismatches 17; Indels
              APPLICATION NUMBER: US/08/894,818B
FILICO BATE: 20-MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/UP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
MANEY
                                                                                                                                                                                                                                             NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: TAKAKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-894-8188-14
                                                                                                                                                                                                                                                                                                                            TELEPRONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SED ID NO: 14-
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CURRENT APPLICATION DATA:
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1104 CGCCCGGCGCGGCGACAAA;#GGCCACGCACCCACGTCGCCTCGATCGCGGCGGCGGCA 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 GGTCGACCCCCTACGATGHCMAGGACACGGAACCCACGTTGCGGGTATCGTTGCCGGAA 531
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                                                                                                                                                                                  ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NUMER: US/09/514,340
FILING DATE: 39-Feb.2000
CLASSIETCATION OPERATOR
PRIOR APPLICATION DATA:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., #800 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.7%; Score 191.6; DB 4; Best Local Similarity 54.5%; Pred. No. 7.1e-30; Matches 583; Conservative 0; Mismatches 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORION NUMBER: 09/000,016
FILING DATE: Jailary 30, 1998
ATTORNEY AGENT THORNATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REPRENCE/COCKET VUMBER: <URKNOWN>
TELECOMMUNICATION INFURBATION:
TELEPRONE: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: genomic_DNA ORIGINAL SOURCE: ORGANISM: Streptomyces antibioticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CONTROL CDS CO
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 Dasg pairs
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IDENTIFICATION METHOD:
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                                                                                                                       STATE: D.C.
COUNTRY: U.S.A.
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Patent No. 5351987
GENERAL INFORMATION:
APPLICANT: Akira ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC REAL HYDROLAGE ACTIVITY FOR 4-SUBSTITUTED 1,4-DHHYDROPYRIDINE ITS EXPRESSION PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1797 cesecceenrecasceceancaaescerrecascascascersarescesacecestrece 1856
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                                                   ACCCGAACCACCCCGATCTGAAGGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCA 571
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CORRESPONDENCE ADDRESS:
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990 GG---TCCGCCGGCTACCACGCCAAGGGCGTGAAGATCGCCGTCCTGGACACCCGGTGTCG 1046
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4.4%; Pred, No. 1.4e-29;
V.A. 0; Mismatches 440; Indels
                                                                                                                                                                     NAME: Warren H. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEPRA: 202-721-8250
                                          FILING DATE: January 30 12
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ 1D NO: 33: SEQUENCE CHARACTERISTICS; LENGTH: 2539 base palre TYPE: nucleic acid STRANDEDNESS: double
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) IDENTIFICATION METHCH
US-09-000-016-3
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Matches 582; Conservative
      CURRENT APPLICATION DATA:
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1164 CGGGCGCCCAGTCCAAGGGCAAGTACAAGGGCGTCGCACCCGGCGCGCGGATCCTCAACG 12233
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                                        689 TCAAGGTTCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCATCATCGCGGGGTGTTGACT 7.8
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Patent No. 614341
GENERAL INFORMATION:
GENERAL ARISAMA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HTS EXPRESSION PRODUCT
TITLE OF INVENTION: HTS EXPRESSION PRODUCT
CORRESSED WENGERS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
STREE: 2033 K Street, N.W., 1800
STREE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
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COMPUTER: IM COMPELIALE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDDEFECT 5.1
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MEDIUM TYPE: Diskett
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1446 CCGGCAGCGCGACGCCCCTCACCGTCGACGACGACGACGAGACAAGCTCGCCG, 1,505
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1392 GCGTCCTGTTCGCCATCGCGGCCGGCAACGAGGGCCCG-----GAGTCGATCGGTTCGC 1445
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                                                                                                                                                                   929 CCGCCGCCGCGAGGAGGTCATAACCGTCGGTGCAGTTGACAGCAACGACAACAACAACAACAACAAA
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Search completed: November 2, 2002, 11:26:38 Job time : 72.5 secs

OM nucleic - nucleic search, using sw model Run on:

November 2, 2002, 10:33:33; Search time 51.5 Seconds (without alignments) 12789.264 Million cell updates/sec

US-09-841-553-2 1977 1 ATGAAGAGGTTAGGIGCTGT......AGGCCGICGTCTACTACGGG 1977 Title: Perfect score: Sequence:

IDBNTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

310279 seqs, 166577418 residues Searched:

Minimum DB seq length; 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Natch 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:

Database :

1. (cgn2_6/ptodeta/7/pubpna/US07_puBCONB.seq:*
2. (cgn2_6/ptodeta/7/pubpna/US07_puBCONB.seq:*
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13. (cgn2_6/ptodeta/2/pubpna/US10_puBCONB.seq:*
14. (cgn2_6/ptodeta/2/pubpna/US10_pubcO

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence (1. Appl Sequence (2. Appl Sequence (3. Appl Sequence (10. Appl Sequence (10. Appl Sequence (10. Appl Sequence (2. Appl Sequence (3. Appl Description US-10-090-624-11 US-10-090-624-15 US-10-090-624-15 US-09-864-761-20241 US-09-864-761-1471 US-09-864-761-19241 US-09-864-761-19241 US-09-864-761-19241 US-09-864-761-19241 US-09-864-761-2513 US-09-887-576-784 US-09-974-300-1934 US-09-974-300-1934 US-09-974-300-1934 US-09-216-393-340 US-09-216-393-340 US-09-216-393-340 US-09-216-393-340 US-09-216-393-340 US-09-216-393-343 % Query Match Length DB Result No.

Sequence 345, Apple Sequence 5, Appl Sequence 12, Appl Sequence 12, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 23, Appl Sequence 3, Appl Sequence 3, Appl Sequence 14, Appl Sequence 11,	Sequence 3, Appl1 Sequence 20699, A Sequence 7694, Ap Sequence 8, Appl1
US-09-216-393-345 US-09-748-033-5 US-09-934-060A-22 US-09-934-060A-22 US-09-934-060A-23 US-09-934-060A-23 US-09-934-060A-23 US-09-934-060A-23 US-09-934-060A-3 US-09-9476-242-3 US-09-476-242-3 US-09-476-242-3 US-09-476-242-3 US-09-476-242-3 US-09-476-242-3 US-09-476-242-3 US-09-476-242-3 US-09-476-242-3	US-09-864-761-20699 US-09-815-242-7694 US-09-748-033-8
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ALIGNMENTS

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SENDICANT: TARKURA, HIKETUL

APPLICANT: SHINGON, TOGACKÓ

APPLICANT: SABDA, KIYOZO

APPLICANT: SABDA, KIYOZO

APPLICANT: KATO, IKUNGSALIO

TITLE OF INVENTION: SYSTEM CO. EXPRESSING HYPERTHERMOSTABLE

TITLE OF INVENTION NUMBER: US/10/090,624

CURREWT FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-06-10

NUMBER OF SEO ID NOS: 33

SOFTWARE: PALENTLY WEFELO: E.O

SEO ID NO 11

LENGTH: 1977 Sequence 11, Application US/10090624 Patent No. US20020132335A1

TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Synthetic US-10-090-624-11

0; Gaps Query Match
100 (1: Score 1977; DB 12; Length 1977; Best Local Similarity 100 (0); Pred. No. 0;
Matches 1977; Conservative 0; Mismatches 0; Indels 0;

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1 ATGAAGAGGTTAGGTGCTGT34 NCCTGCACTGGTGCTCGTGGGTCTTCTGGCCGGAACG 60 ô 임

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121 GGACTGCTGACCCCGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGAACGAGGAAGTG 180 ò

_	Qy 1261 GACATCGCCTAC	DD 1261	OY 1321 GCCAAGCTCAC 	. 0y 1381	Db 1381	3 A	0y 1	Db 1501 GGCTTCGAG Qy 1561 AGCTACAAG	DD 1561	Qy 1621 TCCGCGCGCCGC	1681	1681	DD 1741 GTCAACAGGG	Dy 1801 CTCGACCTCT	Db 1801 CTCGACCTC	qq	Oy 1921 GCCTACAGCA	•	RESULT 2 US-10-090-624-15 ; Sequence 15, Appli		5.4			·	GO: SEQ ID NO 15 LENGTH: 1962 GA TYPE: DNA	
	GGACTGCTGACCCCGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGAAGCAGGAAGTFG	1. GACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGACAGGGGCGTTAAGGTACTCAGG, 240 [GACACCGTCATAATGTTCGGGAACTACCGAGAAAAAAGGGAAAAAAAGGGCGCGGTTAAAAAAAA	241 CTCATGGGCGCCCAGGTCAAGATACTCCTAGATAATCCCTGCTGTCGCGGTTAAATA 300	301 AAGGCCAGGARCTICTGCIGATCGCGGCATGATAGACACGGGTTACTICGGTAACAG 360 	AGGSTCTCGGGGRATAAGTTCATACAGGAGGATTACAAGGTTCAGGTTGACGACGCCACT	AGGGTCTCGGGCATAAAGTTCATACAGGAGGATTCAAGGTTCAGGGTTGACGACGCCACC	421 TCCGTCTCCCARATACGGCCGAFACCGTCGAAACTCCCTCGGCTACGAAGGGGT 480	1 GTGGTGGTTGCCATCGTCGATACGGGTATAGACGCGAACCACCGGATCTGAAGGCAAG \$ 60 CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT			601 GGBACCCACGTTGCGGGGTATCGTTGCCGGAACCGCAGCGTTAACTCCCAGTAACATAGGC 660 601 GGBACCCAACTGCAGGGTATCGTTGCCGGAACCGGCAGCGTTAACTCCCAGTAAATAGGG 660 601 GABACCCAGTTGCCGGGAACCGGCAGGGGGGTAACTCCCAGTAAATAGGG 660	GTCGCCCGGCGGCGAAGCTCGTCGGCGTCAAGGTTCTCGGTGCCGACGGTTCGCGAAGC		721 GICTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTACGGGATA 780 	781 AGGGTCATCAACCTCTCCCTCGCTCCCAGAGGTCCGAAGGAACCGACTCCCTCAGT 8400	AGGGTCATCAACCTCTCCCTCGGGCTCCTCAGAGCTCCGGAACCGAACCGACTCCTCAGT	841 CAGGCCGTCAACAACGCCTGGGACGCCGGTATAGTAATCTGCGTCGCCCCCGGCGGCAAAAACCAGCAAGAAGGCAGGC		961 GEAGTTGACGACAACAACAACAACAACAACAACAAAAAAAAA	021 AGGCTCAAGCCGGAAGTCGTCCCCCGGCGTTGACATCATAGCCCCGCGCGCCCAGCGGA 1980 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	021 AGGCTCAAGCCGGGAAGTCGTCGCCCCGGGCGTTGACATACCCCCCCC		1141 ACCCGGACGTTTCGGGGGTTGGCGCGCTCATCCTCCAGGCCCACCCGAGCTGGACCCCCC. 1203 1141 ACCCGGAGGTTTCGGGCGTTGGGCGCTCATCCTCCAGGCCCACCGAGCTGGACCCCC. 1203	GACAAGGTGAAGACCCCCCTCATCGAGACCCCCGACATAGTCGCCCCCAAGGAGATAACC4 32	
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Sequence 15, Application (%, 100°00624)
patent No. US20020132335A1
GENERAL INFORMATION
APPLICANT TARANGIAN, HIMATE
APPLICANT: SHTWOO, TOMONO
APPLICANT: ASTAM, Kiyozo
APPLICANTON NUMBER: US/10/090,624
CURRENT APPLICATION NUMBER: US/202
PRIOR PILING DATE: 1997-12-05
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 33
SEGURARE: BALEND APPLICATION NUMBER: SUS997
PRIOR FILING DATE: 1997-06-22
NUMBER OF SEQ ID NOS: 33
SEGURARE: PALEND APPLICATION NUMBER: SUS997
PRIOR PILING DATE: 1997-06-22

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                                                                                                                                                                                                                                                                                                                               107 AGAAGAACTATGGTCTGCTAACGCCAGGACTGTTCAGAAAAATTCAAAAATTGAATG6
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                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAGGAAGTGGACACCGTCATATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGTCCAGAACAAGGACAAGTACGGGATAAGGGTCATCAACCTCTCGCTTCGGCTCCTCCC
                                                                                                                                                                 Length 1962;
                                                                                                                                                                                                                                Indels
                                                                                                                                                              Score 750.2; DB 12;
Pred. No. 1.6e-163;
0; Mismatches 618;
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                              37.9%;
Similarity 64.7%;
19; Conservative
                                                                  OTHER INFORMATION: Synthetic
US-10-090-624-15
                                                                                                                                                                 Ouery Match
Best Local Simi
Matches 1219;
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                     1052 ACTGGATAATTGCTGCCAGAGCAAGTGGAACTAGCATGGGTCAACCAATTAATGACTATT
                                           ACACCAAGGCCTCTGGAACCAGCATGGCCACCCGCACGTTTCGGGCGTTGGCGCGTCA
                                                                                       1172 TCCTCCAGGCCCACCCGAGCTGGACCCCGGACAAGGTGAAGACCGCCCTCATCGAGACCG
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; Sequence 2, Application US/10090624
: Fatent No. US20020132335A1
: GENERAL INFORMATION:
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APPLICANT: TARAKURA, HIMATU
APPLICANT: MORISHITA, MAC
APPLICANT: SHIMOJO, TOMOKO
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                                                                                                                                                                                                                                                                                                     Score 560.4; DB 12; Length 1236;
Pred. No. 5.5e-120;
0; Mismatches 371; Indels 3;
APPLICANT: ASADA, Kiyozo

APPLICANT: KATO, IKUNOSHIN

TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERBNCE: TARRAKURA-6

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT FILIKG DATE: 2002-03-06

PRIOR APPLICATION NUMBER: 15:969/1997

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATCHIN VOS: 33
                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                      Query Match 28.3%;
Best Local Similarity 68.0%;
Matches 796; Conservative
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-10-090-624-2
                                                                                                                                                                                    ID NO 2
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Sequence 2021, Application 19/09864761
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Sequence 2021, Application 19/09864761
Sequence 2021, David R.
APPLICANT Rank, David R.
APPLICANT Rank, David R.
APPLICANT Chen, Wensheng Stroke-Derive Stroke Service Control of Sequence 2021, David R.
APPLICANT Chen, Wensheng Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control
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840 TATCGTAAAGCCAGATGAAATAGCCGATATAGCCTACGGTGCAGGTAGGGTTAATGCATA
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FILING DATE: 2001-01:30
PPLICATION NUMBER: PET/USOL/00662
FILING DATE: 2001-01:30
APPLICATION NUMBER: PET/USOL/00661
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5.7%; Score 111.8; DB 10: Length 1635;
Best Local Similarity 44.88; Pred. No. 6.1e-17;
Hatches 514; Conservative 0; Mismatches 627; Indels 6; Caps
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OTHER INFORMATION: EXPRESSED IN LOWG, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA; SIGNAL = 8.6
OTHER INFORMATION: EXPRESSED IN HELIO, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BEAT, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN FORTAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FORTAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
US-09-864-761-20241
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-10-21
PRIOR PLING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
SEQ TO NO SEQ ID NOS: 49117
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RGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G:
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Patent No. US20020048763A1
GENERAL INFORMATION:
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1806 CCTCTACCTCTACGACCCCAANGGCAACCTCGTTGACAGGTCCACGTCGACGACAACAGTA 1865
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                                     1326 GCTCACCTICACCGGCTCCGTCGCCGACAAGGGAAGCGCCACCCACACCTTCGACGTCAG
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5.7%; Score III.8; DB 10; Length 1973;
Best Local Similarity 44.8%; Pred. No. 6.4e-17;
Matches 514; Conservative 0; Mismatches 627; Indels 6;
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN HEACHINA, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9
OTHER INFORMATION: EXPRESSED IN HEARI, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HEARI, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BITAL LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BOUT LIVER, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
                                                                                                                                                                                                                                                                                                                                                                           SCOID NO 3471
  PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PLICATION NUMBER: PCT/USO1/00662
PRIOR PLICATION NUMBER: PCT/USO1/00662
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 69/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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ORGANISM: Homo sapiens
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Length 2712; DB 10; DEBERGAL LINCOMANTAL BLOOMWAY, ROXANDA W.
APPLICANT: Broadway, ROXANDA W.
APPLICANT: GONGOLA, CARMEDIA E
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TITLE OF INVENTION: EFFECT SIS ENDOCHITINASE AND CHIT
FILE OF INVENTION: BROOD, SECONDA PLANT GROWTH
FILE REFERENCE: 19603/3091
CURRENT APPLICATION NUMBER: \$\(\text{(172,003)}\)
PRIOR FILING DATE: 1999-12 \$\(\text{(372,003)}\)
PRIOR FILING DATE: 1999-12 \$\(\text{(372,003)}\)
NUMBER OF SEO ID NOS: 8
SOCIEMARE: PATENTION OF 2.1 ñ 104. GRGANISM: Streptomyces albadoflavus US-09-748-033-4

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                                           GCGAAGCTCGTCGGCGTCAAGGTTCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCATC 732
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 Pred. No. 3.9e-15;
0; Mismatches 698;
Best Local Similarity 45.2%;
Matches 591; Conservative
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4.9%; Score 97.8; DB 10; Length 1075;
Best Local Similarity 46.0%; Pred. No. 9e-14;
Matches 452; Conservative 0; Mismatches 517; Indels 14;
                                                                                                                                                                                                                    EXPRESSED IN HEART, SIGNAL - 18
EXPRESSED IN BRAIN, SIGNAL - 21
EST_HUMAN HIT: AV73979.1, EVALUE 1.00e+00
NT HIT: AL163201.2, EVALUE 2.00e-19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                   OTHER INFORMATION: MY OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
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1785 TACTICCTACA--AGGACTCGACCTCTACGACCCCAACGGCAACCTCGTIGAC 1842
1665 CCCGACCACCCACACCCAGACCTTCACCGGTTCCGTTAACGACTACTGGGACACCAGCGA 1724
                                                                                                                  PRIOR FILING DATE: 2000-02-45.

PRIOR FILING DATE: 2000-02-45.

PRIOR FILING DATE: 2000-05-45.

PRIOR FILING DATE: 2000-05-45.

PRIOR PELING DATE: 2000-05-45.

PRIOR PELING DATE: 2000-05-45.

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PRIOR FILING DATE: 2000-05-45.

PRIOR FILING DATE: 2001-01-46.

PRIOR FILING DATE: 2001-01-34.

PRIOR PELING DATE: 2001-01-36.

PRIOR PELING DATE: 2001-01-30.

PRIOR FILING DATE: 2001-01-30.

PRIOR PELING DATE: 2001-01-30.

PRIOR FILING DATE: 2001-01-30.

PRIOR PELING DATE: 2001-01-30.
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CURRENT APPLICATION NUMBER: U3/09/864,761
CORRENT FILING DATE: 2001-35-23
PRIOR APPLICATION NUMBER: U5:50/180,312
PRIOR FILING DATE: 2000-02-64
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Best Local Similarity 46.0%; Pred. No. 9.7e-14;
Matches 452; Conservative 0; Mismatches 517; Indels 14; Gaps
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OTHER INFORMATION: MAP TO ALO78472.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 27

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 34

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN HELA. SIGNAL = 28

OTHER INFORMATION: EXPRESSED IN HELA. 43

OTHER INFORMATION: EXPRESSED IN HELAGENTA, SIGNAL = 20

OTHER INFORMATION: EXPRESSED IN HELAGENTA, SIGNAL = 25

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 25

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 18

US-09-864-751-2513
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Sequence 7, Application US/9990399

Patent No. US2020038000A1

GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig

APPLICANT: Tuerk, Craig
APPLICANT: Tuerk, Craig
APPLICANT: Thibnow, David
APPLICANT: Smith, Jonathan's D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/CI-C00, 2001, 02-22
PRIOR APPLICATION NUMBER: 09/197,649
PRIOR PILING DATE: 1998-11-23
PRIOR PILING DATE: 1992-01-31
PRIOR PILING DATE: 1992-01-31
PRIOR PILING DATE: 1992-01-31
PRIOR PILING DATE: 1990-08-02
PRIOR FILING DATE: 1990-08-02
SPRIOR PILING DATE: 1990-08-02
                                                                                                                                                               1785 TACTTCCTACA -- AGGACCTCTACCTCTACGACCCCAACGGCAACCTCGTTGAC 1842
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                                                     CACCTTCACCATGAACGTCAACAGGGTGCCAACAAAAAACGGGTGACCTGACCTTCGA 1784
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                                                                                                                                                                                                                                                                                1843 AGGTCCACGTCGAGCAACAGCYA 1865
                                                                                                                                                                                                                                                                                                                      423 CACACTGCACTGATCCACCACTA 401
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238 TICGIGICCGACGACGICGCCICGACGCCGACCGCIGCAAGGIGCICGTCAACAICGAG. 297
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                                                                                                                                                                                                                     APPLICANT: Buckettly.

APPLICANT: Buckettly.

APPLICANT: Brown. D.

APPLICANT: Chang, H.

APPLICANT: Ann, T.

APPLICANT: Ann, T.

APPLICANT: Han, B.

APPLICANT: Han, B.

APPLICANT: Han, B.

APPLICANT: Cooper, Bret.

TILE OF INVENTION: Promoters for regulation of plant expression FILE REPERENCE: 1360.001031

CURRENT APPLICATION: NUMBER: US/09/887,576

CURRENT APPLICATION NUMBER: US 60/213,848

PRIOR FILING DATE: 2000-06-23

PRIOR PLLING DATE: 2000-06-23

PRIOR PLLING DATE: 2000-06-23

PRIOR PLLING DATE: 2000-06-23

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 875

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.9e-10;
0; Mismatches 456; Indels 6;
                                                                                                                                                      Sequence 784, Application US/09887576 Patent No. US20020144047A1 GENERAL INFORMATION:
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Best Local Similarity 45.3%;
Matches 383; Conservative (
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; ORGANISM: Oryza sativa
US-09-887-576-784
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1349 CCGACAAGGGAAGCGCCACCCAACATTCGACGTCAGCGGCGCCCACCTTCGTGACGGCCA 1408
                                                                                                                               1726 ACCTTCACCATGAACGTCAAAAGCGGTGCCACCAAGATAACCGGTGACCTGGACCTTCGAT 1785
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1666 CCGACCACCGCCAGACGTTCACCGGTTCCGTTAACGACTACTGGGACACCAGCGAC 1725
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                                                             718 TTCGTCATCGCCGCGCCCCAAAGGCGCCGGCCTCACCGGCCGCAAGATCATCATCGAC 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS FILE OF INVENTION: OF COLDS CANCER AND METHODS FOR THEIR USE UNRENT ADDITIONAL 20111.471013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: 05/09/922,217
CURRENT FILING DATE: 2001-06-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windóws Version 4.0
SEQ ID NO 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocquence 1058, Application US/05922217
Patent No. 0S20020076414A1 S.
GENERAL INFORMATION:
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US-09-922-217-1058
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US-09-922-217-1058
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US-09-833-263-1058
Sequence 1058, Application US/09833263
Patent No. US20020110547A1
SEQUENCE 11 NPORMATION:
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolik, John A.
APPLICANT: Clapper, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND FILE REFERENCE: 21012-1471C12
CURRENT APPLICATION NUMBER: US/09/833, 263
CURRENT PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SEQ ID NO 1058
SEQ ID NO 1058
LENGTH 15720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gran O.
5920 CCAACCAGGACACCATCACCACCACCAACGCTGAACCCCAACCCAACGCGC 3579
                                                                           TCGACGTCGTCACCGACGCGTCAGCCAGCCAGCGGCGCGCAACCCGAATCCAAACC 1648
                                                                                          1649 CCAACCCGAACCCAACCCGACACGACACCCAAGACCTTCACGGGTTCCGTTAACGACT 1708
                                                                                                                                    1709 ACTGGGACACGACGACGTTCACCATGAACGTCAGGGGGGGCGCGCAGATAACGG,1768
                                                                                                                                                                                                         1769 GIGACCTGACCTTCGATACTTCCTACAACGACCTCGACCTCTACCTCTACGACGCCAACG 1828
                                                                                                                                                                                                                                                   1829 GCAACCTCGTTGACAGGTCCACGTCGAGCAACAGCTACGAGCACGTCGAGTACGCCAACC 3888
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Andrews
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4.2%; Score 83.2; DB 10; Length 15720;
Best Local Similarity 46.2%; Pred. No. 4e-10;
Matches 277; Conservative 0; Mismatches 323; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo saplens
US-09-833-263-1058
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1589 TGGACGTCGTCAGGGAGGGGTCAGCCAGTCCGGCGGCGGGAACCGGAATCCAAACC 1648
                           CCAACCCGAACCCAACCCCSACCACGACACCCAGACCTTCACCGGTTCCGTTAACGACT 1709
                                                                                                     ACTEGGACACCAGEGACCTTCACCATGAACGTCAACAGGGGTGCCACCAAGATAACCG 1768
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4.1%; Score 80.6; DB 10; Length 1329;
Best Local Similarity 49.24 Pred, No. 8.5e-10;
Matches 406; Conservative 7.0; Mismatches 359; Indets 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1934, Application 35/09974300
FORTHORMATION
FORTH DELATA Application 35/09974300
GENERAL INFORMATION
FORTH DELATA SAINT
FORTH CLAUSEN IN GLOUCH
FILLE OF INVENTION EXPENSAL IN EXPENSAL
FILLE OF INVENTION EXPENSAL INFORMATION
FILLE REPERRACE: 10061.500.05
FOURERY FILING DATE: 2001.10.05
FRIOR APPLICATION NUMBER 05/05/05
FRIOR APPLICATION NUMBER 05/05/05
FRIOR PILING DATE: 2000.10.05
FRIOR PILING DATE: 2000.10.05
FRIOR FILING DATE: 2001.0.27
NUMBER OF SEQ ID NOS: 8481
SEQ ID NO 1934
FRIENCE FREEEN FREEEN FREEEN 4.0
LENGTH 1329
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Sequence 6, Application US/0974£033

Sequence 6, Application US/0974£033

Patent No. US20020069431A1

GENERAL INFORMATION

APPLICANT: Broadway, ROXANNE, H.

APPLICANT: Broadway, ROXANNE, H.

TITLE OF INVENTION: EFFECT OF SNDCHITINASE AND CHITOBIOSIDASE AND THEIR

TITLE OF INVENTION: EFFECT OF SNDCHITINASE AND CHITOBIOSIDASE AND THEIR

TITLE OF INVENTION: EFFECT OF SNDCHITINASE AND THEIR

FILE REFERENCE: 19603/3091

CURRENT PELLING NUMBER: US/09/748,033

CURRENT PELLING DATE: 20000.12-23

PRIOR FILING DATE: 1999-12:23

NUMBER OF SED ID NOS: 8

SOFTWARE: Patentin Ver. 2.%

LENDAR OF SED ID NOS: 8

LENDAR OF SED ID NOS: 8
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llarity 46.4%; Pred. No: 9e-10;
Conservative 0; Mismatches 456;
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Fatent No. US/0020146721A1
GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: BERYO, Randy M.

APPLICANT: GLAUSEN, ID GTOTH

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OP INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-03-27

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Pred. No. 8.5e-10;
0; Mismatches 350;
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-974-300-5249
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sst Local Similarity 45.1%;
tches 288; Conservative
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Search completed: November 2, 2002, 13:08:29 Job time : 97.5 secs

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GenCore version 5.1.3
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ALIGNMENTS

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DEFINITION	ENTERTON TO STORE STD ENTERT TO STD STD STD STD STD STD STD STD STD STD
-	similar to contains element TARI reportitive element
	sequence.
ACCESSION	BM161864
VERSION	BM181884.1 GI:17512842
KEYWORDS	EST.
SOURCE	zebrafish.
ORGANISM	Danio rerio
	Eukaryota; Netazoa; Chordata: Cranjata: Vartehrata: G.::
	Actinopterygli, Meopterygli: Telegate! Ostarionbus!
	; Cyprinidae; Danio.
REFERENCE	1 (bases 1 to 641)
AUTHORS	Clark, M., Johnson S. L., Lehrach, H., Lee, R., 1, 5
	S. Hillier, L. Cucaba, T. Martin, J. Bock, C. Woller, Book
	, K., Steptoe, M., Theising, B., Allen, M. Bouers, Frank, J. Wilderwood
	Swaller, T., Gibbons, M., Pape, D. Harrey, N. Cohine B.
	Kohn, S., Shin, T., Jackson, Y., Cardenas M. McCann D. Latter E.
	and Wilson, R.
TITLE	Washu Zebrafish EST Project 1998
JOURNAL	Unpublished (1998:
COMMENT	Contact: Stephen L. Johnson
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501 St. Coule Mo Gaine
	Tel: 314 286 1820
	Fax: 314 286 1910
	Email: zbrafishevarson west! od
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_pro:*

en_gss_mam:* en_gss_mus:*

SUMNARIES

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Query

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BM18184 fv51b11.y AL193990 Tetradon B67199 CpG0015B Cp B67194 CpG0015B Cp AV110415 Zeb mays AV318606 AV938606

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Description

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This sequence is a single read and was generated as part of a large scale clone-rad diequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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/note-*@cmoscope sequence ID : COAG262DD07LP1-end : 17*
105 c: 170 g 282 t 50 others
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46.8%; Pred. No. 7.7e-08;
tive 20; Mismatches 196;
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//db_host="bitloB (phage resistant)"
//note="vector: pwn185-Fi3: Site_1: Draill (CACCATGTS);
Site_2: Drail! (CACTGTGTG); lst strand cDNA was primed
with an oligo(dT) primer [ArdTGGGCTTTTTTTTTTTT];
double-stranded cDNA was liqated to a Draill adapto:
(TGTTGGCTACTGG), digested and cloned into distinct Draill
sites of the pwn185-Fi3 vector (5' site cACTGTGT), 3' site
CACCATGTG, XDIS should be used to isolate the CDNA-
insert. Size selection was performed to exclude fragments
/ Skb inhorary constructed and domated by Dr. Sumio
Sugano (University of Tokyo Institute of Medical Science).
CUSTCGCTCTAAAACTGCG and 3' end primer
CGACTGCAGAGGCGCG.

18 a 214 c 37 g 152 t
Inbrary constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Centericione distribution information can be found through the I.W.A.C.E. Sequencium/LLM. send email to: info@image.llnl.gov
Seq primer: 13 Er from Amersham
High quality sequence stop: 527.
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4.7%; Score 93.4; DB 13; Length 641;
Best Local Similarity 47.7%; Pred. No. 2.7e-09;
Matches 274; Conservative 0; Mismatches 301; Indels 0;
                                                                                                                                                                                                                                                                                                                                            /clone="5412044"
/clone_lib="Sugano SJD adult male"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     issue_type-"whole body"

    641
    /organism="Danio rerio"
    /db_xref="taxon:7955"

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Length 681; Indels 349

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ö 윱 ò 8 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 3 B67199

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE COMMENT

小金銭

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Dread wheat.
Triticum aestlyum's
Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Trachoophyta;
Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Trachoophyta;
Spermerophyta; Idigious,
1 (bases 1 to 140)
Anderson, O.D. (Choi, D.W., Close, T.J., Fanton, R.D., Han P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 25-AUG-2000
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Contact: 01th Anierson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Wester: Regional Research Center
800 Buchanan Street. Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHEN'SS-1758_H21_H21ZS Wheat pre-enthesis spike cona library BE637787 Triticum aestivum cona clone WHE1755-1758_H21_H21, mRNA sequence. BE637787 G::9370898
                                                                                                                       1539 AACCTGGACGGTCAAGGTCGTCAGCTACAAGGGCGGGGGAAGTACCAGGTCGACGTCGT 1598
                                                                                                                                                                                                                                                          1599 CAGCGACGGGAGCCTCAGCCAGTCCGGGGGGGCAACCCGAATCCAAACCCGAACGCGAA 1658
                                                                                                                                                                                                                                                                                                                                                                                         1659 CCCAACCCGGACCACGACACCAGACTTCACCGGTTCCGTTAACGACTACTGGGACAC 1718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1779 CTTCGAFACTTCCTACANTSACCTCGACCTCTACGTCTACGACCCCAACGGCAACGTCGT 1838
                                                                                                                                                                        61 CAACTACTACTACCACTACACTACAACTACAACTACAACTACAACTACCACTACGACTA 120
                                                                                                                                                                                                                                                                                               1839 TGACAGGTCCACGTCGAGCAACAGCTACGAGCACGTCGAGTACGCCAACCGGGCCCGGG 1898
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/organish**Priticum aestlvum*
/oultus***Chindee Spring*
/db.xref**:axon:4565*
/clone="Wasel755-1756_1121_H21*
/clone=Ilb**Wheat pre-enthesis spike CDNA library*
/tissue_type**Spike before anthesis*
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San Francisco General Hospital-University of California, San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciyptosporidium parvum.
Ciyptosporidium parvum.
Ciyptosporidium parvum.
Ciyptosporidium parvum.
Ciyptosporididae; Ciyptosporidium.
1 (basea 1 to 500)
Strong W B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome; a Rexpessed sequence tag and genome survey sequence enalysis 20183851
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                                                                                                                                                                                              1645 AACCCCAACCCCAACCCCAACCCCACCCAACACCAACACCTTCA 1690
                                                                                                                                                                                                                                       San Francisco, CA 94143-0811, USA
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Location/Qualifiers
1. 500
/organism="Cryptosporidium parvum"
/strain="IOHA"
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Bource

FEATURES

BASE COUNT

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/clone_lib**Maize Mapping Project/DuPont Cornsensus
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                          /dev_stage="Adult plant"
//de_host="E. col1 SOLR"
//de_host="E. col1 SOLR"
//de_host="E. col1 SOLR"
//de_host="E. col1 SOLR"
//de_host="E. col1 Sole"
//def_corn Lambda Uni-Lap XR, excised phagemid:
//def_corn Lambda Uni-Lap XR, excised phagemid:
//def_corn Lambda Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns rinmed, white; green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a conA library was made, and
poly(A) RNA were prepared, a conA library was made, and
poly(A) RNA were prepared, a conA library was made, and
phagemids in the TJ Close lab (Choi; Close, Fenton) at
phagemids in the TJ Close lab (Choi; Close, Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (All other authors).
//development
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PAC
clade, Panicoldeae, Andropogoncae, Zea.
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Halney, C.F., Dolan, M., Mido, G.H., Vogel, J.M., Whiteitt, WS Arthur, L.W., Hanafey, M., Morgante, N. and Tingcy, S.V.
Arthur, L.W., Hanafey, M., Morgante, N. and Tingcy, S.V.
Arthur, L.W., Hanafey, M., Morgante, N. and Tingcy, S.V.
Naize Mapping Project/DuPont Consensus Sequences for Design Of Major Probes
Unpublished (2002)
2 (bases 1 to 1116)
2 (bases 1 to 1116)
2 (bases 1 to 1116)
2 (bases 2 to 1116)
3 (bases 3 to 1116)
3 (bases 3 to 1116)
3 (bases 4 to 1116)
4 (bases 4 to 1116)
5 (bases 5 to 1116)
5 (bases 6 to 1116)
5 (bases 7 to 1116)
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/db_xref="MalzeDB:632501"
/db_xref="taxon:457"
/clone="CL57831_1"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacese; Pooldeae

1 (bases 1 to [212)
Sato, R., Saisho, Dg. and Takeda, K.
Barley EST sequenching project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shinoi
Center For Genetic Figure of Genetics
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Anote—'this sequence is part of a project of EST assembles resulting from the application of public contigs tr, seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the worsto addressing of BACs in conjunction with the Maize Mapping Project 43 of 220 the 43 others
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@esuss.nig.ac.jp.
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greenlouds. Whole spike with awns trimmed, white, green
and yellow anher were collacted and total RNA, and
propintal collacted and total RNA, and
the CDNA clones were in vivo exclased to give philasesript
phagemids in the TJ Close lab (Chol, Close, Fanton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors).

30 a 172 c 148 g 72 t
                         800 Buchanan Street, Albany, CA 94710, USA Tal: 510559573 Fax: 5105595818. Fax: 5105595818. Email: candersniew.usda.gov
This EST was generated by sequencing from the 3' end of the cl
Sequences have been trimmed to remove vector sequence and low guality sequence with phred score less than 20.
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WHE1798_B12_D242T Wheat pre-anthesis spike cond library Triticum estivum cond wHe1798_B12_D24, mRNA sequence.
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1 (bases I to 482)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Haia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,G.T., The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
/db_xref="taxon:77009"
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/clone_lb="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
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/tlssue_type="top three leaves"
/dev_stage="adult, heading stage"
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Services, Pacific West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1095 CCCGATAAACGACTACTACACCAAGGCCTCTGGAACCAGCATGGCCACCCCGCACGTTTC 1154
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AZ046831 750 bp DNA linear GSS 16-MAR-2000 nbeb0088017r CUGITR:ce BAC Library (ECORI) Oryza sativa genomic clone OSJNBb0088017r. DNA sequence. AZ046831 SECORI)
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Spermatophyta; Nagroliophyta; Lillopsida; Poalas; Poacaa;
Ehrhartoidese; Orycaae; Oryca,
                                                                                           979 AACATCGCCAGCTTCTCCAGCAGGGACCGAGGGG-----ACGGAAGGCTCAAGCG 1032
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                                                                                                                            261 GGCACGGAGTCGTACAGCTTGCCTCCGGCACGTCCATGGCCGCCCCCCACGTC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                       321 ACCGCRTCGTGCGCTCGTGAAAAAGGGGAACCGGACTGGTCGCCGTCAAG 380
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Ouery Match 5.9%; Score 77.2; DB 14; Length 482; Best Local Similarity 55.4%; Pred. No. 5.7e-06; Matches 173; Conservative 0; Mismatches 133; Indels 6
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REFERENCE AUTHORS

JOURNAL COMMENT

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E 1 (bases 1 to 750)
S Wing, R. and Dean, R.A.

Ming, R.A. and Dean, R.A.

L Unpublished (1998)
Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Email: winggetemson.edu
Seq primer: GCTATTTAGGTGACACTATAG
Class: BAC ends
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Location/Qualifiers
1.750
/organism="oryza sativa"
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/oranymy.me"Triticum aestivum"
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Hestern Regional Research Center
800 Buchanan Street Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B0753023 1022 A06_A122S Wheat salt-stressed root cDNA library friticum aestivum cDNA clone WHE4122_A06_A12, mRNA sequence.
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Spermatophyta; Magroliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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Email: candersofpw usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence wich phred score less than 20
Seq primer: SK primer.
Location/Qualiflers
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BQ753023.1 GI:21930805
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Fax: 5105595818
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made from poly-A RNA in the Clones to be sequenced were
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Hordeum vulgare.
Eukaryota, Vitadiplantae; Streptophyta; Embryophyta; Trachsophyta;
Spermatophyta; Magnellophyta; Liliopsida; Posles; Posceae; Pooldeae
; Triticeae; Hordeum;
1 (bases 1 to 6#5)
Hedley, P., Liu, F.; Caldvell, D., McCallum, N., Mudle, S., Cardle, L.,
Ramssy, L., Mart.ay, G., Marshall, D.F. M. and Waugh, R.
Development of Satley Transcriptome Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ753506 645 bp mRNA linear EST 26-JUL-2002 EBBn01_SQ004_HO7_R enther, yellow stage, no Creatment, cv Optic, EBBn01 Hordeum vulgare CDNA clone EBBn01_SQ004_H09 5', mRNA
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                                                                                                                               Length 422;
                                                                                                                Query Match 3.8%; Score 75.8; DB 13; Length Best Local Similarity 54.5%; Pred. No. 1.1e-05; Matches 152; Conservative 6.9; Mismatches 127; Indela
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Contact: Wangland R. Marshall DF
Genome Dynamicas/Computational Biology
Scottish Crop Research Institute
Invergowria, Dunière, D2 5DA, Scotland, UK
Tel: 00 44 1382 %2731
Fax: 00 44 1382 %2735
Fax: 04 44 1382 %2745
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/organism-"Hordeum vulgare"
/cultivare Optic"
/db_xref_"teaton.6513"
/clone="SEan01_S0004_H09"
/clone_like-anther, yellow st
               Site 3: EcoRI; The library cloning vector lambda ZAP I prepared by mass excision.
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/dev_strue="yellow stage"
/lab_hopt="DH108"
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1 (bases 1 to 422)

Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt
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                                                               1487 ACACCGCCTACTACGCCTTCGAGAAGGTCGGCTACTACAAGCCGACCGCGGAACCTGGA 15546
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/organism="Sorghum bicolor"
/ordarae="Brx623"
/db_xrefe"taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda 2ap II; Site_1: Xhor;
                                                                                                                                 1547 CGGTCAAGGTCGTCAGCTACAAGGGCGCGGCGAACTACCAAGGTCGACGTCGTCAGCGAAG 1506
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                                                                                                                                                                                                                                                                     1663 ACCCCACCACCACACCACACCTTCACCGGTTCCGTTAACGACTACTGGGACACCAGC 1722
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                    277 GAACCGGATTCGCCGCCCCCCAAGATGAACGCCACCTCAACGGCCCCGCCCTCATCGGCT 336
                                                                                                                                                          514 GGGGGTACAGCAACTTCAACGGCGGCAACGAGGGGGTGAAGAGCTACTTCAACAAGTCC 573
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Contact: Cordonider-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Fint Sciences Building, Rm. 2502, Athens, GA 30602-7271, USK.
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Sorghum bicolor
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ALIBORATE STATES OF SEQUENCE.

GSS: genome survey sequence.

Tetracdon nigroviridis

Tetracdon nigroviridis

Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euraleogtomi;
Actinoptergii; Neoptergii; Teleostei; Bueleostei; Neoteleostei;
Acanthomorpha; Acanthoptergii; Percomorpha; Tetracdontiformes;
Tetracodontidae; Tetracodor

Tetracodontidae; Tetracodor

Secondoria, Fizames; C. Mincker, P., Brottier, P., Quetier, F., Sautin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis; insing Tetracodon nigroviridis DNA sequence

L Unpublished

P. Aracoa 1 - 7771.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigre=ir-dis genome. For more information, please take a look at http://www.genocope.cns.fr/Tetraodon.

Location/Qualifiers
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                                                                                                                                                                  1106 ACTACTACACCAAGGCCTCTGGAACCAGCATGGCCACCCCGCACGTTTCGGGCGTTGGCG 1165
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                                                                                                        3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 IGGICTACGACCTCGGCGTGGGCGACTACAGCGCCTACATCTGCGCGCTGCTCGGCGAGG: 313
                                                                                                                                                                                                                                        cereal IGF (Investigating Gene Function) project
                                                                      Length 645;
                                                                      Score 75.6; DB 14; Length Pred. No. 1.3e-05; 0; Mismatches 134; Indels
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Triticum monococcan
Triticum monococcan
Enkaryota, Viridiantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiantae, Streptophyta; Editopsida; Poales; Poaceae, Pooldeae;
Spermatophyta; Magaraliophyta; Editopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticam;
I (bases to 61%).
Anderson, O.D., Graco, S., Dubcovsky, J., Echenique, V., Han, P.S., Hsla
Anderson, O.D., Graco, S., Miller, R., Rausch, C.J., Sealon, C.L.,
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/db_xref="lcaton:99883"
/clone=*199624"
/clone=ib="62"
/note="chic*:0ope sequence ID : COAG199BB12LP1-end : T7"
/ 265 cold = 69 g 184 t 45 others
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493 ATCGGCAGCCGGCCAGCAACAACAACAGCAGCAACAACTTCAGCGGGTACGGGGG 552
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University
Unpublished (1999)
Contact: Walbor V
Department of Blaicgleal Sciences
Stanford University
855 California A.6. Palo Alto, CA 94304, USA
Fax: 650 723 222;
Fax: 650 723 222;
Email: walbot@stanford.edu
Plate: 660033 From: P column: 06.
Location/Qualiflers
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                                                                                      Unpublished (2001)
Contact: Olin Anderson
Contact: Olin Anderson
Contact: Olin Anderson
West Area, Western Regional Research Center
B000 Buchann Street, Albany, CA 94710, USA
Fax: 5105595818
Eax: 5105595818
Exati: candersnépw.usda.gov
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Stamova, B. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Early reproductive apex cDNA library from Tritition
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AW453236 559 bp mRNA linear EST 17-FEB-2000 mRNA sequence. Wixed stages of anther and pollen Zea mays cDNA, AW453236 GIESP4222 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magroliophyta; Lillopsida; Poales; Poacese; PACC clade; Panicoidesu; Andropogonese; Zea, (bases Lo.55); Andropogonese; Zea, Walbot.V. /note-forgan; anthers; Vector: Lambda 2ap; Site_1: EcoRI; Site_2: Xhc;; Anther and pollen cDNA library.
Directionally sequenced with 5' and at the EcoRI site.
Created by Anie Franklin.*
1 198 c 177 g 178 t /db_xref*_taxon:6577"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poateae; Pootdeae;
Triticaes; Hordeum.
1 (bases 1 to 607)
Hichalek, M., Weschke W., Pleissner, K.-P. and Graner, A.
BST sequencing and analysis in barley
Unpublished (2000)
Contact: Stell Nils
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Institute of Plant Genetics and Crop Plant Research (IPK)
Correnstr . 0.04466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
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ALIGNMENTS

RESULT 1 AAT85667

				Protease; research reagent: thermal stability; thermococcus celer; ss.					
AAT85667 standard; DNA; 1977 Bp.		20-APR-1998 (first entre	Thermococcus protease coding sequence,	earch reagent; thermal stab	caler DSM-Ze			96WO-JP0325	95JP-03232(F
AAT85667 atan	AATB5667;	20-APR-1998	Thermococcus	Protease; res	Thermococcus calar DSM-36	WO9721823-A1.	19-JUN-1957	07-NOV-1996;	12-DEC-1995;

(TAKI) TAKARA SHUZO CO LED! 74×27×2×4×

Asada K, Kato I, Mitta M, Morishita M, Takakura H; Tsunasawa S, Yanamoto K;

WPI; 1997-332794/30. P-PSDB; AAW24121.

Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and are

us-09-841-553-2.rng

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GGAACCCACGTTGCGGGTATCGTTGCCGGAACCGGCAGCGTTAACTCCCAGTACATAGCC 660 CAGGCCGTCAACAACGCCTGGGACGCCGGTATAGTAGTCTGCGTCGCCGCCGGCAACAGG 990 80 5 GTCTCCACCATCATCGCGGGTGTTGACTGGGTCCACACAACAAGGACAAGTACGGGAT# 720 This sequence represents the coding sequence for the protease from Thermococcus celer DSM-2476. This sequence encodes a protease of the invention have extremely high thermal stability. The proteases of the invention have extremely high thermal industriality. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries. TCCGTCTCCCAGATAGGGGCCGATACCGTCTGGAACTCCCTCGGCTACGACGGAAGGGGT 480 540 540 9 <u>وون</u> 240 240 CTCATGGGCGCCGGGGCAAGTACTCCTACAAGATAATCCTGCTGCTGTGGCGGTTAAAATA 300 AAGGCCAGGGACCTTCTGCTGATCGCGGGCATGATAGACACGGGTTACTTCGGTAACACA 360 AGGICTCGGGCATAAAGITCATACAGGAGGATTACAAGGTICAGGTTGACGACGCCAÇÎ : 420. 120 121 GGACTGCTGACCCGGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGAACCAGGAAGTG 180 120 Sdeb ATGAAGAGTTAAGGTGCTGTGGTGCTGGCACTGGTGGTCGTGGGTCTTCTGGCCGGAACG 60 GTGGTGGTTGCCATCGTCGATACGGGTATAGACGCGAACCACCCCGATCTGAAGGGCAAÄG CTGGTGCTTGCCATCGTCGATACGCTATAGACGCGAACCACCCGATCTGAAGGGAAG GTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGACCCCTACGATGACCAGGGACAC GTCGCCCCCGCCGCGAAGCTCGTCGGCGTCAAGGTTCTCGGTGCCGACGGTTCGGGAA& GCCCTTGCGGCACCCGTAAAACCGGTTGTCAGGAACAACGCGGTTCAGCAGAAGAACTAC GACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTAAGGTACTGAGG DB 18; Length 1977; ö Indels Sequence 1977 BP; 453 A; 659 C; 554 G; 311 T; 0 other; ö reagents Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1977; Conservative 0; Mismatches Page 86-87; 159pp; Japanese as research and industrially useful 721 721 781 781 661 541 541 601 601 661 301 361 421 431 481 481 301 361 61 121 181 181 241 241 a g ద 윱 õ g ò ò ò õ a ð 유 δ g g ò 8 윰 ŏ ద ò g ð ò ð ò g

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AGCIACGAGCACGTCGAGTAKKCCAACCCCGGCCCGGGAACCTGGACGTTCCTCGTCTAC 1920 HITHIHIHIHIHIHIHIHIK STAGGCGCCCGGGGAACCTGGACGTCCTCGTCAAC 1920 1620 1620 CTCGACCTCTACCTCTACGP:::CCAACGGCAACCTCGTTGACAGGTCCACGTCGAGCAAC 1860 1680 1680 1740 1740 1560 1560 1380 1440 1440 1500 1500 1320 1320 1380 1140 1140 1200 1200 1260 1260 1080 1080 1020 1020 GCCIACAGCACACGGCTGGGGGGCCCCCCCAGGCCGTCGTCTACGGG 1977 CAGACCTTCACCGGTTCCG%%AACGACTACTGGGACACCAGCGACACCTTCACCATGAAC GGCTTCGAGAAGGTCGGCJAAGTAACCCGACCGCAACCTGGACGGTCAAGGTCGJC GACAAGGTGAAGACCGCCCTCATCGAGACCGCCGACATAGTCGCCCCCCAAGGAGATAGCG GACATCGCCTACGGTGCGGGTAGGGTGAACGTCTACAAGGCCATCAAGTACGACGACTAC GGGCCGAACACCTACACCGT.CGGCTCACCGCCGCCGCGAGCAAGGTCATAACCGTCGGT HELLITTELLITTELLITTELLE STREET TO THE TELLITTELL AGGCTCAAGCCGGAAGTCGT@@@CCCGGGGGTTGACATCATAGCCCCGGGGGCCAGCGGA ACCAGCATGGGCACCCCGATALACGACTACTACACCAAGGCCTCTGGAACCAGCATGGCC GCAGTTGACAGCAACGACAA&NYCGCCAGCTTCTCCAGCAGGGGACCGACCGCGGACGGA 1601 1561 1621 1681 1681 1741 1741 1921 1561 1621 1801 1861 1861 1261 1321 1381 1381 1441 1441 1501 1321 1201 1261 1021 1081 1081 1141 1141 1201 901 961 1021 196 841 901 a 셤 ŏ 유 ð S ŏ 음 ö ð 8 g ò g ò 8 õ a ö ò a g à 윱 셤 5 ð g ö 8 8 a 3 8 ò õ

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The invention relates to a hyperthermostable protease derived from a thermophilic becterium (especially Pyrococcus furiosus). The protease has working temperature 40-110 deg-C (optimum 80-95 deg-C), working pH-5-10 et 95 deg-C), and retains more than 90% of its activity after, 3 hours polypeptide of formula SiG-Ala-Cly-Cly-Asn-PRO, where SiG is a signal polypeptide of formula SiG-Ala-Cly-Cly-Asn-PRO, where SiG is a signal peptide from subtilisin, and PRO is the above protease whost cells genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable. For industrial use, can be used as an additive for drugs, washing agence and foodstuffs and for chemical synthesis.
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Tsunasawa S, Yamamoto K;
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                                                                                                                                                                                                                                                                                          170 ACCAGGAAGTGGACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTA 229
                                                                                                                                                                                                                                                         This sequence represents the coding sequence for a a protesse of the invention. The protesses of the invention have extremely high thermal stability. The protesses can be used as research respects, and industrially in the food, wing and chemical industries.
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                       68.68; Score 1360.8; DB 18; Length 1977; 83.98; Cred, No. 7.3e-242; Live. 0; Mismatches 292; Indels 9; C
                  Protease(s) and genes encoding them obtained from Thermococcus Pyrococcus strains - have extremely high thermal stability and useful industrially and as research reagents
                                                                                                                                                              Sequence 1977 BP: 527 A: 562 c; 513 G; 375 T; 0 other;
                                                                        Claim 11; Page 95-97; 159pp; Japanese.
                                                                                                                                                                                                                     Conservative
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P-PSDB; AAW24123
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Best Local Simil
Natches 1573; C
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                    GACCGACCGCGGACGCAAGGCTCAAGCCGGAAGTCGTCGCCCCCCGGGGGTTGACATCATAG 1063
                                                               CCCCGCGCGCCAGCGGAACCAGCATGGGCACCCCGATAAACGACTACTACACCAAGGCCT 1123
                                                                       1124 CTGGAACCAGGATGGCCACCCCGGACGTTTCGGGCGTTGGCGCGGTCATCCTCCAGGCCC 1183
TCGCCGCCGCCAACACGCGGCCGAACACCTACACCGTCGGCTCACCCCGCCGCCGCGGAGCA. 943
                                                                                                 ACCCGAGCTGGACCCCGGGACAAGGTGAAGACCGCCCTCATCGAGACCGCCGACATAGTCG 3243
                                                                                                                          1184 ACCGAGCTGGACCCCGGACAAGTGAACACGCCCTCATCGAGACCGCGGGGTA43
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                                                                                                                                                                        TCAAGTAGGACGACGAAGGTCACGTTCACCGGCTCCGTCGCCGACAAGGGAAGCG 1363
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This sequence represents a fragment of the coding sequence for the processe from Thermococcus celer DSN-2476 (see AAT85667 for full length sequence). This sequence excodes a fragment of the processe of the invention. The processes of the stability. The processes can be used as research reagents, and industrially in the fooc. Erry and chemical industries.
                                                                                                   Protease, research reagent; thermal stability; thermococcus celer; 89.
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                                                                                                                                                                                                                                                                                       Morishica N, Takakura H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1859 BP; 420 A; 531 C; 509 G; 299 T; 0 other;
                                                                         Thermococcus protease fragment coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 112-113; 159pp; Japanese.
AAT85677 standard; DNA; 3859 BP.
                                                                                                                                                                                                                                                                                Asada K, Kato I, Mitta M,
Tsunasawa S, Yamamoto K;
                                                                                                                                                                                                         96W0-JP03253
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                                                                                                                           Thermococcus celer DSM-2476.
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                                                                                                                                                WO9721823-A1.
                                                 20-APR-1998
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Pyrococcus furtosus hypersteermostable protease gene - useful for recombinant prodn. of hypersthermostable protease
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13-JUN-1994;
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                                                                                                               1293 CTACAAGGCCATCAAGTACGACGACGACGAGCCCAAGCTCACCTTCACCGGCTCCGTCGCCGA 1352
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                              CTACTGGGACACGGGCTCGAGCGACATCGACCTCTACCACCACCCCAACGGAAACGA
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Protease; research reagent; thermal stability; thermococcus celer; ss.

Thermococcus celer DSM-2478

409721823-A1

19-JUN-1997.

Thermococcus protease Inagment coding sequence.

(first entry)

20-APR-1998

AAT85679;

AAT85679 standard; DNA; 3454 BP.

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               DB 17, Length 898;
                                        526 GATCTGAACGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGACCCCCAAC 585
                                                                  GTCATAACCGTCCAGTTGACAGCAACGACAACATCGCCAGCTTCTCCAGCAGGGGA 1005
                                                                                                                                                                                                                                                                                          CCGCGCGCCAGCGGAACCAGCATGGGCACCCCGATAAACGACTACTACAACCAAGGCCTCT 1125
                                                                                              TCCCAGTACATAGGCGTCGCCCCGGCGCGAACCTCGTCGGCGTCAAGGTTCTCGGGTGTL 7 (6.5
                                                                                                      CCGAGCTGGACCCCGGACAGGTGAGACCGCCCTCATCGAGACCGCCGACATAGTGGC
                                                                                                                         GACGGTTCGGGAAGCGTCTCCACCATCATCGCGGTGTTGACTGGGTCGTCGTCAGAAGAAG 765
                                                                                                                                 GACAAGTACGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCTCCCAGAGCTCCGACGGA .825
                                                                                                                                                           ACCGACTCCCTCAGTCAGGCCGTCAACACGCCTGGGACGCCGGTATAGTAGTCTGCGTC 825
                                                                                                                                                                                      1126 GGAACCAGCATGGCCACCCGCACGTTTCGGGCGTTGGCGCGCTCATCCTCCAGGCCCAC 1185
                                                                                                                                                                                                                                                                                                                                                                           1146 CCCAAGGAGATAGGGGACATCGCCTAGGGTGGGGTAGGGTGAAGGTGAAGGCTACAAGGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                       AAGTACGACGACTACGCCAAGGTCACCTTCACGGCTCCGTCGCCGACAAGGGAAGCGCT 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 CCGACCGCGGACGGAAGGCTCAAGCCGGAAGTCGTCGCCCCCGGCGTTGACATCATAGÇC
               Score 833.2; DB 17; Length
Pred. No. 1.1e-144;
0; Mismatches 24; Indels
  C: 266 G: 130 T: 11 other;
               Query Match
Best Local Similarity 97.0%;
Matches 874; Conservative (
Sequence 898 BP; 192 A; 299
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Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and are useful industrially and as research reagents

Disclosure; Page 114-115; 159pp; Japanese.

I, Mitta M. Morishita M. Takakura

(TAKI) TAKARA SHUZO CO 1220.

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Asada K, Keto I, Mitta m Tsunasawa S, Yamamoto K; WPI; 1997-332794/30.

96WO-JP03353.

77-NOV-1996; 12-DEC-1995;

95JP-0323288

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This sequence represents a fragment of the coding sequence for the protease from Thermococcus celer DSM-2476 (see AAT85667 for full length sequence). This sequence encodes a fragment of the protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research rengents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947 AAGSCCAGGGACCTTCTGCTGA~CGCGGGATGATAGACAGGGTTACTTCGGTAACACA 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCTTCCGGCACCCGTA AACCGGTTGTCAGGAACAACGCGGTTCAGCAGAAGAACTAC 120
                                                                                                                                                                                                                                                                                                                                                                                           181 GACACCGTCATAATGTTCG%GAGCTACGGAGACAGGGACAGGGGGGTTAAGGTACTGAGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACTGCTGACCCCGGGACXGTTCAAGAAGTCCAGAGGATGAACTGGAACCAGGAAGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CTCATGGGCGCCCAGGTCAAGTCCTTACAAGATAATCCCTGCTGCTGGCGGTTAAAATA 300
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                                                                                                                                                                                                                                                                            301 AAGGCAGGGACCTTCTGCTGAACGGGGGATGATAGACACGGGTTACTTCGGTAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 AGGGTCTCGGGCATAAAGTTC@ExsAGGAGGATTACAAGGTTCAGGTTGACGACGCCACT
                                                                                                                                                                                          Ouery Match
40.8%; Score 806.8; DB 18; Length 1464;
Best Local Similarity 95.1%; Pred. No. 8.5e-140;
Matches 811; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                              Sequence 1464 BP; 352 A 352 C; 403 G; 357 T; 0 other;
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                                                            grgfiggtigccatcgtcgatacgggtatagacgcgaaccacccgatctgaagggcaag (540) 📳
                                                                                                                     Protease; research reagent; thermal stability; pyrococcus furiosus; as
                  11067 TCCGTCTCCCAGATAGGGCCGATACCGTCTGGAACTCCCTCGGCTACGAACGGAAGGGGT(126
                                                                                                                                                                                                                                           661 GTGCCCCCGGGGGGAAGCTCGTCGGCGTCAAGGTTCTCGGTGCCGAACGTTCTGGAAGC 7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the coding sequence for the protease from Pyrococcus furiosus DSM-3638. This sequence encodes a protease of the invention have extremely high thirmal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                     GGAACCCACGTIGCGGGTATCGTTGCCGGAACCGGCAGGGTTAACTCCCAGTACATAGGC 660
                                                                                Protease(s) and genes encoding them obtained from Thermococcus, Pyrococcus strains - have extremely high thermal stability and useful industrially and as research reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus furiosus PFUS protease coding sequence
                                                                                                                                                                                                                                                                                                                                                                                    AGGGTCATCAACCTCTCCCTCGCCTCCCAGAGCTC 1464
                                                                                                                                                                                                                                                                                                                                                                     AGGGTCATCAACCTCTCCCTCGGCTCCTCCCAGAGCTC 818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT85695 standard; DNA; 1962 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furiosus DSM-3638
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P-PSDB; AAW24129.
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                                                        AGGTACTGAGGGCTCATGGGCGCGCGCCAGGTACTCCTACAAGATAATCCCTGCTGTCG
                                                                                                                                               CGGTTAAAATAAAGGCCAGGGACCTTCTGCTGATCGCGGGCATGATAGACACGGGTTACT
                                                                                                                                                                                                                                    335 GGGGTAAAGCTAAAGCTTCAGGGGTTAAGGTTTATCCAGGAAGACTACAAAGTTACAGGTTA
                                                                                                                                                                                                                                                                                                            ACTCCTCGGCTACGACGGAAGCGGTGTGGTTGCCATCGTCGATACGGGTATAGACG
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                                                                                    ACCAGGAAGTGGACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTA
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                      Indels
Ouery Match 37.94; Score 750.2; DB 18; Best Local Similarity 64.79; Pred. No. 2.36-129; Matches 1219; Conservative 60; Mismatches 618;
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1112 ACACCAAGGCCTCTGGAACCAGCATGGCCACCCGGCACGTTTCGGGGGGTTTGGCGCGCTCA 1171
                                                                                            1172 PCCTCCAGCCCAGCCGAGCTGGACCCCGGACAAGGTGAAGACGGCCTCATCGAGACCG 1231
                                                                                                                             1232 CCGACATAGTCGCCCCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAGGG 1291
                                                                                                                                                                                                                            1292 TOTAGAAGGCCATCAAGTACGACGACTAGGCCAAGGTCACCTTGAGGGCTCCGTCGGCGGT351
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The invention relates to a hyperthermostable protesse derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protesse has working temperature 40-110 deg-C (optimum 80-95 deg-C), working pH 5-10 at 95 deg-C. The invention and then 90 of its activity after 8 hours polypoptide of formulas SG-Ala-Cly-Cly-And-PRO, where SIG is a signal pettide from subtiliasin, and PRO is the above protesse Host cells pettide from subtiliasin, and PRO is the above protesse Host cells genes are used for the recambing trouble of the protesse. The hyperthermostable protesse which can be prepared in quantity suitable for industrial use, can ha used as an additive for drugs, washing agents and foodstuffs and for chamical synthesis.
                                                                                                                                                                                                                                                                  Recombinant hyperthermostable protease from Pyrococcus furiosus -
and gene encoding it, for large scale production of the protease for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 AGAAGAACTAGGGACTGGTGACCCCGGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGA 169
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                                                                                                                                                                                                     Takakura
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                                                                                                                                                                                                    Shimojo T,
                                                                                                                                                                                                                                                                                                                            Disclosure; Page 59-60; 81pp; Japanese.
                                                                                                                                                                                          Asada K, Kato I, Horishita M,
                                                                                                       98WO-JP52465
                                                                                                                                                           (TAXI ) TAKARA SHUZO CO LTD
                                                                                                                                    97JP-0151969
                                                                                                                                                                                                                      WPI; 1999-080907/07.
               Pyrococcus furiosus.
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                                                                                                                                 10-JUN-1997;
                                         WO9856926-A1.
                                                                                                    04-JUN-1998;
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                              1652 ACCCGAACCCAACCCGACCACGACGACCTTCACCGGTTCCGTTAACGACTACT
                                                                                                                                                               AGCTCAAGGCCGTCGTCTACTACGG 1976
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P-PSDB; AAW24122.
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                                                                              692 AGGITCTCGGIGCCGACGGITCGGGAAGCGICTCCACCAICATCGCGGGIGIIGACTGGG 75]
                                                                                                           512 CITCTCATCCAGATCTCCAAGGAAAAGTAATTGGGTGGGTAGATTTTGTCAATGGTAGGA 511
                         GCAGCG---TTAACTCCCAGTACATAGGGTCGCCCCGGGGGAACTCGTCGTCGGCGTCA-69}
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               575 CGACCCCTACGATGACCAGGGACACGGAACCCACGTTGCGGGTATCGTTGCCGGAACCG
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This sequence represents the coding sequence for the protease from pyrococcus furiosus DSM-1618. This sequence encodes a protease of the invention. The proteases into the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food on the communical industries.
                                                    83
                                          Protease; research reagen;; thermal stability; pyrococcus furiosus;
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Pyrococcus strains - have extremely high thermal stability and
useful industrially and ps research reagents
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/note= "সমূত= Gly, Val"
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Pyrococcus furiosus protemse coding sequence.
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35.0%; Score 692.8; DB 18; Length 1566;
Best Local Similarity 67.1%; Pred. No. 8.6e-119;
Matches 1020; Conservative 0; Mismatches 483; Indels 18; Gaps*
                                                                             459 CCTCGGCTACGACGGAAGCGGTGTGGTTGCCATCGTCGATACGGGTATAGACGCGAA 528
                                                                                               60 CTTGGGATATGATGGTTCTGGAATCACAATAGGAATAATTGACACTGGAATTGACGCTTC 119
                                                                                                                                                 120 TCATCCAGAATCTCCAAGGAAAAGTAATTCGCTGGTAGATTTTGTCAATGGTAGGAATA, 179
                                                                                                                               519 CCACCCGATCTGAAGGGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGAC 578
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                  Query Match
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                                 TGACTACTCCTACACCGC NACTACGGCTTCGAGAAGGTCGGCTACTACAACCCGACCGC 1535
                                                      1536 CGGAACCTGGACGGTCAAGGTCGTCAACGGCGCGCGCGAACTACCAGGTCGACGT 1595
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and gene encoding it, for Estge scale production of the protesse for
industrial use.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyperthermostable proteass "ragment encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1956 CAAGGCCGTCGTCTACTAGG 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX05920 standard; DNA; :236 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1545 GACGCTAAAGTTTATGG 1565
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P-PSDB; AAW94836.
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Query Match
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                 the invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40-110 deg-C (optimum 80-95 deg-C), working PH-5-10 (optimum 6-9), and retains more than 90% of its activity after 8 hours at 95 deg.C. The invention also provides gene sequences encoding a polypeptide of formula SIG-Ala-CHY-GHY-ABA-FRO, where SIG is a signal peptide from subtilisin, and PRO is the above protease. Host cells genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foodstuffs and for chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1055 CATCATAGCCCCGCGCCCAGCGAACCAGCATGGGCACCCCGATAAACGACTACTACAC MAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             996 CAGCAGGGGACCGACGGCGCACGGAAGGCTCAAGCCGGAAGTCGTCGCCCCCGGCGTTGX 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1116 CAAGGCCTCTGGAACCAGCATGGCCACCCGCACGTTTCGGGGGGTTGGCGCGCTCATGCT 11/5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 nGCRAGCRAAGTRATTACAGTTGGAGCGTTGACAAGTATGATGTTATAACAAGCTTGTG 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCGACGGAACCGACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGAACGCCGGTATAGT 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                         639 CG---TTAACTCCCAGTACATAGGCGTCGCCCCCGGCGCGAAGCTCGTCGGCGTCAAGGT 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 CCACCCCGATCTGAAGGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGAC 578
                                                                                                                                                                                                                                                                                                                                                                                                                    638
                                                                                                                                                                                                                                                                                                    459 CCTCGGCTACGACGGAAGCGGTGTGGTTGCCATCGTCGATACGGGTAIAGACGCGAA 518
                                                                                                                                                                                                                                                                                                                               CITGGGAIAIGAIGGITCIGGAAICACAAIAGGAAIAAIIGACACIGGAAIIGACGCIIC 119
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       579 CCCCTACGATGACCAGGGACACGGAACCCACGTTGCGGGTATCGTTGCCGGAACCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AGCAAGTAATGGGAAGTACAAGGAATGGCTCCAGGAGGTAAGCTGGCGGGAATTAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
28.3%; Score 560.4; DB 20; Length 1235;
Local Similarity 68.0%; Pred. No. 2.1e-94;
hes 795; Conservative 0; Mismatches 371; Indels 3; G
                                                                                                                                                                                                                 Sequence 1236 BP; 368 A; 251 C; 309 G; 308 T; 0 other;
Claim 6; Page 37-38; 82pp; Japanese
                                                                                                                                                                                                                                                        Query Mat
Best Loca
Matches
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                                                                                                                                                                                                                                                                                          1536 CGGAACCTGGACGGTCAAGGTC3TCAGCTACAAGGCGGGGGGGGAACTACCAGGTCGACGT
                  CAAGGCCATUAAGTACGACGACGACCAAGCTCACCTTCACCGGCTCCGTCGCCGACAA
                                                                                                                                 GGGAAGCCCCACCCACACCTTTCGACGTCACGGCGCCACCTTCGTGACCGCCACCTCTA
                                                                                                                                                                                                    CTGGGACACGGCCTCGAGGGACATCGACCTCTACCTCTACGACCCCCAACGGGAACGAGGT
                                                                                    Pyrococcus furiosus hyperelibermostable protease gene · useful recombinant prodn. of hyperelibermostable protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 9 pene (AAT08141) that codes for a hyperthermostable protests (AAR87007) of Pyrococcus furlosus 2 DNA sequences (AAT08133-74) are provided encoding peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 564 BP; 121 A; 1195 C; 161 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsunasawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease; hyperthormostable; thermostability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1200 GGTAAGTGATGGTTCCCTTTCACACCTGG 1229
                                                                                                                                                                                                                                                                                                                                                                                                            1596 CGTCAGCGACGGGAGCCTCAGCCAGTCCGG 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 66-67; 85 ptp: Japanese.
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Yamamoto K;
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13-JUN-1994;
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This sequence represents a fragment of the coding sequence for the protease from Thermococcus celer DSM-2176 (see AAT85667 for full length sequence). This sequency encodes a fragment of the protease of the invention. The proteases the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                018 GGAAGGCTCAAGCCGGAAGTCGTCGCCCCCGGCGTTGACATCATAGCCCCGGGCGCGAGC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 CACGGAACCCACGTTGCGGGTNTCGTTGCCGGAACCGGCAGCGTTAACTCCCAGTACATA 657
                                                                                                                                                                                                                                                                                                                                                                                718 AGCGTCTCCACCATCATCGCGCGCGTGTTGACTGGGTCGTCCACAACAAGGACAAGTACGGG 777
                                                                                                                                                                                                                                                                                                                                                                                                778 ATAAGGGTCATCAACCTCTCCCTCGGCTCCCAGAGCTCCGACGGAACCGACTCCCTC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease(s) and genes encours them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and are useful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCGGGCCGAACACOTACACGGTCGGCTCACCGCCGCGCGGGGAGGTCATAACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asymmetric hydrolase, dhpA + substituted-1,4-dlhydropyridine; derivative; Streptomyces *tridosporus; ester; chiral; synthesis;
                                                                                                                                                                                                                     Query Match 26%%; Score 532.8; DB 18; Length 564; Best Local Similarity 97.3%; Pred. No. 2.56-89; Matches 543; Conservative 0; Nismatches 17; Indels 0;
                                                                                                                                                                                           Sequence 564 BP; 121 Applians C; 161 G; 87 T; 0 other;
                                                                          Disclosure; Page 110-112; 159pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                           1078 GGAACCAGCATGGGCACCCCGATAAACGACTACTACCAAGGCCTCTGGAACCAGCATG 1137
                                     CACGGAACCCACGTTGCGGGTATCGTTGCGGGAACCGGCAGCGTTAACTCCCAGTACATA, 657
                                                                                                                                                                                                                                                                                                                                                        GGCGTCGCCCCCCCGCGCAAGCTCGTCGCCGTCAAGGTTCTCGGTGCCGACGGTTCGGGA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease; research reagent; thermal stability; thermococcus celeggies.
                                                                                                     AGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTACGGG
                                                                                                                                                                                                            ATAAGGGTCATCAACCTCTCCCTCGGGCTCCTCCCAGAGCTCCGAACGGAACCGACTCCCTC 2837
                                                                                                                                                                                                                                                                                                     AGCGGGCCGAACACCTACACCGTCGGCTCACCCGCCGCCGCGAGCAAGGTCATAACCGTC 957
                                                                                                                                                                                                                                                                                                                   AGTCAGGCCGTCAACAACGCCTGGGACGCCGGTATAGTAGTCTGCGTCGCCGCCGGCAAG
  Pred. No. 2.5e-89;
0; Mismatches 17; Indels
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Matches 543; Conservative
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Tsunasawa S, Yamamoto K;
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P-PSDB; AAW24126.
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Thermococcus

AAT85676;

RESULT 12 AAT85676

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W09721823-A1

12-DEC-1995;

07-NOV-1996; .9-JUN-1997

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1224 GCAAGGTCCTCGACGTCTGGCGACGACTCCGGCATCTCGCGGCATGGAGT 1283
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338..25.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the Streptomyces viridosporus dhpA gene which encoces an asymmetric hydrolase which acts on 4-substituted-1,4-dhydropyridine derivatives. The ensyme allows the efficient conversion of 4-substituted-1,4-dhydropyridine esters to chiral partially hydrolysed derivatives, for use in the synthasis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 CCGGCAGC---GTTAACTCCCAGTACATAGGCGTCGCCCCCGGCGGAAGCTCGTCGCGCG
cardiovascular, treatment, hypertension; ischaemic heart disease; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

9.7%; Score 191.6; DB 18; Length 2539;

Best Local Similarity 54.5%; Pred. No. 2e-26;

Matches 583; Conservative 0; Mismatches 439; Indels 48; Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATAGACACGGGTTACTTCGGTAACACAAGGGTCTCGGGCATAAAGTTCATACAGGAGG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asymmetric hydrolase gene derived from Streptomyces viridosporus acts on 4-substituted-1,4-di:hydro:pyridine derivatives to produce chiral derivatives useful for synthesis of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isshiki K, Matsufuji M, Nakashima T;
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                                                                                                                              338, 2539
/*tag= a
/note= "no stop codon given"
950, 2509
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/note= "encodes AAW13666"
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                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          96WO-JP02147.
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                                                               Streptomyces viridosporus
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Tsuruta T, Yoshioka T;
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1686 GCGCGCGCGCCTCCTGAAGCAGCACCCCGACCTCGGCCGAACTGAAGGGCG 1745
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derivative. Streptomycas virilosporus. ester, chiral. synthesis.
cardiovascular. treatment. hypertension. ischaemic heart disease.
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                                                                                                                                       1332 IGGACACCGGAGACCCACCGGCTGGAGGCGGCGGCGGTCGACAAGCTGTCGGCCGAGAAGG
                                                                                                                                                                                                                                    929 CCGCCGCCGCGAGCAAGGTCATAACCGTCGGTGCAGTTGACAGCAACGACAACATCGCCA
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GGGTCGTCCAGAACAAGGACAAGTACGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCT
                                                                                                  809 CCCAGAGCTCCGACGGAAC@ACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGACGCCG
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/produc's ChpA_protein_product
/note= *from 5. viridosporus*
2540..2899
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338..2809
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Streptomyces antibioticus
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928

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1046 CCGGCGTTGACATCATÀGCCCCGCGCGCAGCGGAACCAGCATGGGCACCCCGAT---- 1100
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                                                                                                         869 GIATAGTAGTCTGCGTGGCGGCGGCAACAGGGGGGCCGAACACCTACACGCTCGGCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                   Asymmetric hydrolase gene derived from Streptomyces viridospocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1047 ACAGAGCCATCGGGACGTGAAGGCCGGGTGA---CCGCGTCCAAGAACTTCACGCGC 1103
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Beet Local Similarity 54.5%; Pred. No. 2e-26;
Matches 583; Conservative 0; Mismatches 439; Indels 48; Gaps.
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                                                                                                                                                                                                                                                                                                Isshiki K, Matsufuji M, Nakashima T;
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      /*tag= c
/product= Melanin
/note= "from S. antibioticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 37-43; 78pp; Japanese.
                                                                                                                                                                                                    96JP-0067478.
95JP-0212975.
                                                                                                                                                                   96WO-JP02147
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Tsuruta T, Yoshioka T;
                                                                                                                                                                                                                                                           (SACC ) MERCIAN CORP.
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P-PSDB; AAW13668.
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31-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trattgacacaggtatagacggaaatcacgttgacgtctcaggtggaaaaataagat 562
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                                                                                                                                                                                                                                                                  Query Match
9.1%; Score 180.6; DB 23; Length 2121;
Best Local Similarity 55.7%; Pred. No. 2.1e-24;
Matches 395; Conservative 0; Mismatches 299; Indels 15; Gaps
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                             New DNA sequence of thermophilic protein decomposition enzyme and protein derived therefrom -
                                                                                                                                                 This sequence represents the DNA encoding the Thermoanserobacter yonsell subtilisin-like serinc protease of the invention.
                                                                                                                                                                                                                        Sequence 2121 BP; 712 A; 410 C; 425 G; 554 T; 20 other;
                                                                                                              Claim 1; Page 6; 15pp; Korean.
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time 30 Seconds alignments)	AND TO TO THE TOTAL TO THE TOTA		:	747574		•
OM protein - protein search, using sw model Run on: October 31, 2002, 13:25:03 ; Search time 30 Seconds (Without alignments)	TALLe: US-09-841-553-5 Perfect score: 3428 Sequence: 1 MKGLKALILVILVGLYVGS	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 747574 segs, 111073795 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length; 0 Maximum DB seq_length; 2000000000	Post-processing: Minimum Match 0% Maximum Macch 100% Listing first 45 summaries

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	100000000000000000000000000000000000000	tandard; } } (first	research	6; 96WO 5; 95JP KARA SHUZ Kato I, 5, Yamam 332794/30 185669.
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                                                                                                                                                                                                                               GPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASG. 360
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                                                                                                                                                                                            ISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNS 300
               This sequence is a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                IVIVFENHREKEIAVRVLELMGAKVRYVYHIIPAIAADLKVRDLLVISGLIGGKAKLSGV (120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                         1 MAGLKALILVILVILVILGAVVSVAAAPEKKVEQVRNVEKNYGLLTPGLFRKIQKLNPNEELS 60
                                                                                                             .09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reagent; thermal stability; pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDVVSDGSLSQ
                                                                                                                                                                                  RFIQEDYKVTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGIID/GIDASHPDLQGKV
                                                                                                               MKGLKALILVILVIGLVVGSVAAAPEKKVEQVRNVEKNYGLLTPGLFRKIQKLNPNEEIS
                                                                                                                                                          61 TVIVFENHREKETAVRVLELMGAKVRXVYHIPATAADLKVRDLLVISGLTGGRAKLSGV
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                                                                             Length 659;
                                                                                               Indels
                                                                             100.0%; Score 3428; DB 18;
100.0%; Pred. No. 2.3e-209;
iive 0; Mismatches 0;
  Page 92-95; 159pp; Japanese.
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                                                                                                  Conservative
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                                                                                Query Match
Best Local Similarity
Matches 659; Conserv
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                                                                629
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    Claim 9;
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                                                                                                                                                                                                                                                                                              This sequence represents the protease from Pyrococcus furiosus DSM-This sequence is a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can is used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLYLYDPNGNBVDYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYQYDVVSDGSLSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Length 654;
                                                                                                                                                                                                Protease(s) and genes encoding them obtained from Thermococcus Pyrococcus strains - have Extremely high thermal stability and useful industrially and as research reagents
                                                                                                 Ä
                                                                                                   Takakura
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.3% Pred. No. 4.7e-182;
Matches 582; Conservative 22; Mismatches 50;
                                                                                                                                                                                                                                                                     Disclosure, Page 125-128; 159pp; Japanese
                                                                                                   Morishita
96WO-JP03253.
                             95JP-0323285
                                                                 SHUZO CO LID
                                                                                                   Kato I, Mitta M., S., Yamamoto K.
                                                                                                                                                   WPI; 1997-332794/30.
N-PSDB; AAT85695.
                                                                                                                                                                                                                                                                                                                                                                                                          654 AA;
                                                                     (TAKI ) TAKARA
07-NOV-1996;
                                 12-DEC-1995;
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The Invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40.110 deg-C. Optimum 80.95 deg-C), working phi.5-10 at 95 deg-C), working phi.5-10 at 95 deg-C. The invention also provides gene sequences encoding a polypeptide of formula SIG-Ala-Gly-Gly-Asn-PRO, where SIG is a signal peptide from subtiliisin, and PRO is the above protease. Host cellasse (especially Bacillus strains) transformed with vectors comprising the genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing @gents and foodstuffs and for chemical synthesis.
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IGWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGS 240
                                                LOLY LY DPNGNLV DRSTSSNSY EHVEYANPAPGTWTFLVY AYSTYGWADY QLKAVV YG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant hyperthermostable protease from Pyrococcus furiosus and gene encoding it, for large scale production of the protease for industrial use.
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                                                            121 RFIQEDYKVTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGIDASHPDLQGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 654;
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Pred. No. 4.7e-182;
2; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ≅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asada K, Kato I, Morishita M, Shimojo T, Takakura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 60-63; 82pp; Japanese.
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88.3%; Pred
ttive 22; 3
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                                                                                                                                                                                                                                                                                                                                                                                            98WO-JP02465
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                  Hyperthermostable protease
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.39
Matches 582; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-080907/07.
N-PSDB; AAX05929.
                                                                                                                                                                                                                                                                                                        Pyrococcus furiosus.
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                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1998;
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This sequence represents the protesse from Thermococcus celer DSN-2476. This sequence is a protesse of the invention. The protesses of the unvention have extremely high thermal stability. The protesses can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                    TSMGTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIA 420
                                                                                                                           DIAYGAGRUNVYKAIKYDDYAKLTFIGSVADKGSATHTFDVSGATFVTATLYWDIGSSDI 480
                                                                                                                                                                     DLYLYDPNGNEVDYSYTATYGREKVGYYNPTAGTWTVKVVSYKGAANYQVDVVSDGSLSQ 540
                                                                                                                                                                                                            SGGGNPNPNPNPNPTPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDLTFDTSYND 600
                                                                                                                                                                                                                                                     LDLYLYDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLYYAYSTYGWADYQLKAYYYYG 659
                                                                                                                                                                                                                                                                                               ISTIIKGVEWAVDNKDKLÅIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNS
                                         Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thormal stability and are useful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease; research reagent; thermal stability; thermococcus celer,
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Tsunasawa S, Yamamoto K;
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                                                                                                                                                                                                                                                                                                                                                          AAW24121 standard; Protein; 659
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                                                                                                                                                                                                                                                                                                                                                                                                                         Thermococcus protease.
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N-PSDB; AAT85667
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VCVAAGNSGPNTYTVGSRAARSKVITVGAVDSNDNIASFSSRGPIADGRLKPEVVAPGVD 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                               HPDLQGKVIGWVDFVNGRSYPYDDHGHCTHVASIAAGTGAASNGKYKGMAPGAKLAGIKV 232
                                                                                                                                                                                                                                                                                                                                                 114 KAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATYVWN-LGYDGSGITIGIIDTGIDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKGLKALILVILVLGLVYGSVAAAPEKKVEQVRN---VEKNYGLLTPGLFRKIQKLNPNE
                                                                                                                                                                                                                                                                                                     Ouery Match 85.04; Score 2914; DB 20; Best Local Similarity 83.74; Pred. No. 9.4e-177; Matches 558; Conservative 1.47; Mismatches 46;
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                                     Gaps 7.
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                                                         MKGLKALILVILVIGLVVGSVAAAPEKKVEQVRN---VERNYGLLTPGLFRKIQKLNPNE 57
                                                                      HPDLQGKVIGWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGKYKCMAPGAKLAGIKV 232
                                                                                                                                                                            LCADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV 7392
                                                                                                                                                                                                                VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTANGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                                       533 VSDGSLSQSGGGNPNPNPNPNPTPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDL 592
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                                                                                                                                 114 KAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATYVWN-LGYDGSGITIGIIDTGIDAS 172
                                                                                                                                                                                                                                                          VCVAAGNSGPNTYTYGSPAAASKYITYGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
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                                                                                                                                                                                                                                                                                                                                                                                                                     593 TPDTSYNDLDLYLYDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLVYAYSTYGWADYQL 652
                                                                                                                                           IVAPKEIADIAYGAGRVNYYKAIKYDDYAKLIFIGSVADKGSAIHTFDVSGATFVTAILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyperthermostable, protease, thermophilic, bacterium; subtilisia; additive, drug, washing agent; foodstuff; chemical synthesis.
                                          Indels 16
                         Length 659;
                       ; Score 2914; DB 18;
; Pred. No. 9.4e-177;
47; Mismatches 46;
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                       Ouery Match
Best Local Similarity 83.7%;
Matches 558; Conservative 4.
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Gaps 5 28

Indels 16; Length 659;

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The invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40-116-deg-C (optimum 80-95 deg-C), working pH 5-10 (optimum 619, and retains more than 90% of its activity after 8 hours at 95 deg-C. The invention also provides gene sequences encoding a polypeptide of formula SIG-Ala-Gly-Gly-Asn-FRO, where SIG is a signal peptide from subtilisin, and PRO is the above protease. Host cells especially Bacillus strains it transformed with vectors comprising the genes are used for the recombinant production of the protease. The hyperthermostable protease, which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foostuffs and for chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant hyperthermostable protease from Pyrococcus furiosus and gene encoding it, for large scale production of the protease industrial use.
                                                                                                                                                                                                                                                                                        Takakura
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                                                                                                                                                                                                                                                                                        Shimojo
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                                                                                                                                                                                                                                                                                    Asada K, Kato I, Morishita M,
                                                                   98WO-JP02465
                                                                                                                                      97JP-0151969
                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-080907/07.
N-PSDB; AAX05926.
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                                                                   04-JUN-1998;
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17-DEC-1998.
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ASKVITVGAVDSNDNIASFSSRCPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYT 372

DNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAA

253 121 313

61 PYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSTSTGTKGVEWAV 120

373 KASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY 432

361

493

DYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYOVDVVSDGSLSOSGGGNPNPNP

613 VDRSTSSNSYEHVEYANPARGTWTFLVYAYSTYGWADYQLKAVVYYG 659

476

553 NPTPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDLFEDTSYNDLDLYLYDPNGNL 612

KAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEV 492

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AAW94838 standard; Protein; 522 AA
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                                                                                                                                                                                                                                              This sequence represents the protease from Pyrococcus furiosus DSM:363 Inhis sequence is a protease of the invention. The proteases of the Invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                    VSDGSLSQSGGGNPNPNPNPNPTPTTDTQTFTGSVNDYMDTSDTFTMNVNSGATKITGDL 592
                                         593 TFDISYNDLDLYLYDPNGNLVDRSISSNSYEHVEYANPAPGTWTFLVYAYSTYGWADYQL 652
                                                                                                                                                                                           a Alexandra
                                                                                                                                                                                                                                Protease; research reagent; thermal stability; pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and are: useful industrially and as research reagents
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                                                                                                                                                                                                                                                                        Location/Qualiflers
428 .
/label- Gly, Val
/note- "encoded by GNA"
                                                                                                                                                                                                                                                                                                                                                                                                                          Morishita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 87-90; 159pp; Japanese.
                                                                                                                                                    AAW24122 standard; Protein; 522 AA.
                                                                                                                                                                                                              Pyrococcus furiosus protesse.
                                                                                                                                                                                                                                                      Pyrococcus furiosus DSM-3638.
                                                                                                                                                                                                                                                                                                                                                                                                                         Asada K, Kato I, Mitta M,
Tsunasawa S, Yamamoto K;
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                                                                                                                                                                                            (first entry)
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Matches 449; Conservative
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N-PSDB; AAT85668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 AA;
                                                                                           KAVVYYG 659
                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                        W09721823-A1
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AAW24122
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The invention relates rota hyperthermostable protesse derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protesse has working temperature 40-110 deg.C (optimum 80-95 deg.C), working pH 5-10
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                                                                    Hyperthermostable; protesse; thermophilic; bacterium; subtilisin; additive; drug; washing_agent; foodstuff; chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                 Recombinant hyparthermostable protease from Pyrococcus furlosus .
and gene encoding it, for large scale production of the protease
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                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 39-41; 82pp; Japanese.
                                                                                                                               Location/Qualiflers
                                                                                                                                                      /label= Gly or val
                                                                                                                                                                                                                                                                                                   Asada K, Kato I, Norishita M,
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                                                                                                                                                                                                                                                                            (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                    97JP-0151969
                                              Hyperthermostable protease.
                      06-MAY-1999 (first entry)
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                                                                                                         Pyrococcus furiosus,
                                                                                                                                          Misc-difference 428
                                                                                                                                                                                                                                                                                                                                                               and gene encodi
industrial use.
                                                                                                                                                                             WO9856926-A1.
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AAW94838;
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5; Gaps

51; Indels

133 AELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGIDASHPDLGGKVIGWVDFVNGRSY 192

PYDDHGIIGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVDWAV 252

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 (optimum 6-8), and retains more than 90% of its activity after 8 hours at 95 deg C. The invention also provides gene sequences encoding a polypeptide of formula SiG-Ala-Gly-Gly-Asn-PRO, where SiG is a signal peptide from subtilisin, and PRO is the above protease. Host cells genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foodstuffs and for chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity after 8 hours
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                                                                                                                                                                                                                                                                       193 PYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVEWRV 252
                                                                                                                                                                                                                                                                                    DNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAMDAGIVVCVAAGHSGPNTYTVGSPAA 312
                                                                                                                                                                                                                                                                                                                                               121 DNKDKYGIKVINLSLGSSQSSDGTDALSQAVNAAWDAGLVVVVAAGNSGPNKYTIGSPAA 180
                                                                                                                                                                                                                                                                                                                                                                         ASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                            KAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEV 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYSTTATYGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDVVSDGSLSQSGGGNPNPNPN, 552
                                                                                                                                                                                                                                 5; Gap8
                                                                                                                                                                                                                                                                                                                                                                                         373 KASGISMATPHYSGYGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyperthermostable; protease; thermophilic; bacterium; subtilisin; additive; drug; washing agent; foodstuff; chemical synthesis.
                                                                                                                                                               DB 20; Length 522;
                                                                                                                                                                                          51; Indels
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Best Local Similarity 85.2%; Pred. No. 4.5e-141;
Matches 449; Conservative 22; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyperthermostable protease fragment.
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                                                                                                                                      522 AA;
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Best Local S:
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The invention relates to a hyperthermostable protease derived from a thermoballic bacterium (especially Pyrococcus (turiosus). The protease has working temperature 40-110 deg.C (optimum 80-95 deg.C), working pH 5-10 (optimum 6-8), and retains more than 90% of its activity after 8 hours at 95 deg.C. The invention also provides gene sequences encoding a polypeptide of formula SIG-Na-Gly-Nan-PRO, where SIG is a signal peptide from subtilish, and PRO is the above protease. Host cells (especially Bacillus strains) transformed with vectors comprising the genea are used for the recombinant production of the protease. The flyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and footstuffs and for charactal synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 ASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGIDASHPDLQGKVIGWVDFVNGRSY 192
                                                                                                                                                                                                        Recombinant hyperthermostable protease from Pyrococcus furiosus - and gene encoding it, for large scale production of the protease for industrial use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 PYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVEWAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVEWAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AAPGISMATPHVAGIAALLLQAHPSWTPDKVKTALIETADIVKPDEIADIAYGAGRVNAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 KASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKELADIAYGAGRVNVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAIKYDDYAKLTFTGSVÄOKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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89.5%; Pred. No. 7.8e-114;
tive 15; Mismatches 28;
                                                                                                                                  Shimojo T,
                                                                                                                                                                                                                                                                                      Claim 2; Page 35-37; 82pp; Japanese.
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                                                                                                                             Asada K, Kato I, Morishita M,
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97JP-0151969.
                                                                                               (TAKI ) TAKARA SHUZO CO LTD.
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Matches 367; Conservative
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                                                                                                                                                                WPI; 1999-080907/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 AA;
                                                                                                                                                                                    N-PSDB; AAX05920.
                                                              10-JUN-1997;
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ID AAR8
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THE WATER

Takakura H;

05-JUN-1995; 26-JUL-1994; 13-JUN-1994;

famamoto K; Asada K,

W09534645-A1

21-DEC-1995.

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This sequence represents a fragment of the protease from Pyrococcus furiosus DSN-3638 (see AAW24122 for full length sequence). This sequence is a fragment of the protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IDTGIDASHPDLQGKVIGWVDEVNGRSYPYDDHGHCTHVASIAACTGAASNGKYKGWAPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 LVISGLTGCKAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVISGLTGGKAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 IDTGIDASHPDLQGKVICWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASHGKYKGMAPG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease(s) and genes encoding them obtained from Thermococcus Pyrococcus strains - have extremely high thermal stability and useful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.2%; Score 864; DB 18; Best Local Similarity 100.0%; Pred. No. 1.8e-47; Matches 168; Conservative: 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                        Kato I, Mitta M, Morishita M, S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 118-119; 159pp; Japanese.
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                                                                                                                                       96WO-JP03253
                                                                                                                                                                                            95JP-0323285
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94JP-0130236
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                                                                                                                                                                                                                                                      TAKI ) TAKARA SHUZO CC LTD
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N-PSDB; AAV03761.
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                                                                                                                                                                                                                                                                                                                                          Paunasawa S,
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                                                                                                                                       07-NOV-1996;
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13-JUN-1994;
                        WO9721823-A1
                                                                             19-JUN-1997
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                                                                                                                                                                                                                                                                                                           Asada K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 DLQGKVIGWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Invention relates to the hyperthermostable protease of Pyrococcus furiosus and its prodn. as a recombinant protein in transformants using a vector carrying the protease gene (AATO8141). A genomic DNA sequence of the invention is given in AATO8131 and its encoded protein in AAR87009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 ADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.9%; Pred. No. 3.6e-59;
Matches 203; Conservative 9; Mismatches 18; Indels 1: Gans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus furiosus hyper:thermostable protease gene · useful for recombinant prodn. of hyper:thermostable protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 APRASGTSMGTPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKT 405
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                                                                                                                                                                                   /note= "unspecified amino acid"
                  Protease; hyperthermostable; thermostability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 70-71; 85pp; Japanese.
                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              94JP-0173912.
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N-PSDB; AAT08131.
                                                                      Pyrococcus furiosus.
                                                                                                                                                          Misc-difference 196
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8×4×4×4×4×8

AAW24127;

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Indels

Length 168,

13

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Gaps

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DB 18; Length 188;

us-09-841-553-5,rag

Asada K, Yamamoto P

X44X0X444X4X0000XX

Sequence

199 N 259

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379

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This sequence represents a fragment of the protease from Thermococcus celer DSM-2476 (see AAW24121 for full length sequence). This sequence is fragment of the protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research respense and industrially in the food, drug and chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                          61 GIRVINLSLGSSGSSDGADSLSQAVNNAMDAGIVVCVAAGNSGPNTYTVGSPAAASKVIT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                319 VGAVDSNDNIASFSSRGPTADGKLKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 HGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVEWAVDNKDKY 258
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                                                                                                                                                                                                                                                                                                                 2 HGTHVAGTVAGTGSV-NSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asymmetric hydrolase; dhpa; 4-substituted-1,4-dihydropyridine; derivative; Streptomyces viridosporus; ester; chiral; synthesis; cardiovascular; treatment; hypertension; ischaemic heart disease.
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205..724
/note= "fragment of dhpA protein; see AAW13666"
                                                                                                                                                                                                         25.2%; Score 862.5; DB 18; Length 89:4%; Pred. No. 2.6e-47; Ive 8; Mismatches 11; Indels
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Disclosure; Page 110-112; .59pp; Japanese.
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95JP-0212975.
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Tsuruta T, Yoshioka T;
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N-PSDB; AAT61454.
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31-JUL-1995;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GIRVINESLGSSQSSDGADSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVIT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease(s) and genes encoding them obtained from Thermococcus Pyrococcus strains · have extremely high thermal stability and useful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                               Score 862.5; DB 17; Length 188;
Pred. No. 2.68-47;
8; Mismatches 11; Indels 1;
                                                                                                                  useful
                                                                                                                                                                                                           The invention relates to a gene (AAT08141) that codes for a hyperthermostable procease (AAR87007) of Pyrococcus furiosus. 2 DNA sequences (AAT08133-34) are provided encoding peptides (AAR87010-11).
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                     Tsunasawa
                                                                                                                    Pyrococcus furiosus hyper:thermostable protease gene recombinant prodn. of hyper:thermostable protease
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Tsunasawa S, Yamamoto K;
                     Morishita M,
                                                                                                                                                                              Example 4; Page 66-67; 85pp; Japanese
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Best Local Similarity 89.4%;
Matches 168; Conservative 8
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                     Kato I, Mitta M,
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N-PSDB; AAT85676.
                                                                            WPI; 1996-049674/05
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Nakashima T;

07-NOV-1996;

12-DEC-1995;

WO9721823-A1

AAW24126;

RESULT 12

19-JUN-1997.

disease

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cardiovascular; treatment; hypertension; ischaemic heart
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31-JUL-1995;
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                                                                                                                                                                                                                                                                                           21;
                                      This sequence is an asymmetric hydrolase encoded by the Streptomyces viridosporus dhpA gene. The enzyme acts on 4-substituted-1,4-dihydropyridine derivatives. The enzyme allows the efficient conversion of 4-substituted-1,4-dihydropyridine esters to chiral partially of 4-substituted-1,4-dihydropyridine esters to chiral partially substitutes, for use in the synthesis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart
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33.6%; Pred. No. 9.1e-36;
.1ve 62; Mismatches 223; Indels 115; Gaps
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Page 49-55; 78pp; Japanese
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Matches 202; Conservative
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Claim 3;
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This sequence is a fusion protein comprising Streptomyces viridosporus dhpA gene product (an asymmetric hydrolase) winch acts on 4 substituted-1.4 dibydropyriddine daryvatives, and molanin from S. antibioticus. The DhpA enzyma allows the efficient conversion of 4 substituted-1.4 dibydropyriddine esters to chiral partially hydrolysed darivatives, for use in the synthesis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart diseaso.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 LTGGKAKLSGVRFIQEDYKYTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 DASHPDLOGKVIGWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.2%; Score 692.5; DB 18; Length 823; Best Local Similarity 33.6%; Pred. No. 1.1e-35; Matches 202; Conservative. 62; Mismatches 223; Indels 115; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asymmetric hydrolase edie derived from Streptomyces viridosporus acts on 4-substituted-194-di-hydro:pyridine derivatives to produce chiral derivatives useful for synthesia of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTSHPDLKGRVTASKNFTAAPG-AGDKVGHGTHVASIAAGTGAOSKGKYKGVAPGAAILN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 IKVLGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNN-AWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 AGIVVCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGF-TADGRLKPEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGVDIIAPRASGTSMGTPIND----YYTKASGTSMATPHVSGVGALILOAHPSWTPDKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APGVDITAASAEGNDIGOEVGEGPAGYMTISGTSMATPHVAGAAALLKOOHPDWTSAELK
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                                                                                                                                                                                                                                               sednence),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsufujl M,
                                                                             Location/Qualifiers
1.734
/label- DhpA_proteIn_product
                                                                                                                                               Claim 5, Page 37-43; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isshiki K,
Streptomyces viridosporus. Streptomyces antibloticus.
                                                                                                                                                                                                                                                                                                                                                                                                                96WO-JP02147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0067478
95JP-0212975
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N-PSDB; AAT61455.
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Tsuruta T, Yoshioka
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21;

suitable for the treatment of e.g. hypertension and ischaemic heart

520 AA;

Seguence

disease.

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586 TKITGDLFDT-SYNDLDLYLYDPNGNLYDRSTSSNSYBHYEYANPAPGTWTFLYYAYST 544
                                                                                                                                                                                                    180 OX
                                                                                                                     643 LGSGRGYG------APATDTATLRLPKGTYLVDSWIAKDFGTLKGGIDWLVQPKLSV 693
                                                                     583 GGTVDGAYSAYVVATGGGQTVRTAAAVQREVESYDVTVRHIGRDGKPTTEHLTDLIGYAG 642
                                                                                                                                                              526 LIYRNLGTQDVTLKLTSTATDPKGKAAPAGFFTLGATTVTVPA---GGSASVDMTADTRL 582
                                                489 GNEVDYSTTAYIGFEKVGYYNPTAGTWTVKVVSY------KGAANYQVDVVSDGS 537
                                                                                                LSQSGGGNPNPNPNPNPTPTTDTQTF---TGS-VNDYWDTSDTFTM-----NVNSGA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asymmetric hydrolase gene derived from Streptomyces viridosporus? Sets on 4-substituted-1,4-di:hydro:pyridine derivatives to produče? Chiral derivatives useful for synthesis of cardlovascular drugs
/note- "Ser238 as indicated in the specification"
                                                                                                                                                                                                                                                                                                                                                                                      asymmetric hydrolase; dhpA; 4-substituted-1,4-dhydropyridine; derivative; Streptomyces viridosporus; ester; chiral; synthesis; cardiovascular; treatment; hypertension; ischaemic heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Asp19 as indicated in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isshiki K, Matsufuji M, Nakashima T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 60-63; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAW13666 standard; protein; 520 AA
                                                                                                                                                                                                                                                                                                                                                                Fragment of dhpA gene product.
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95JP-0212975
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces viridosporus.
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Tsuruta T, Yoshioka T;
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N-PSDB; AAT61454-55
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Misc-difference
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31-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                    ITVGAVDSNDNIASFSSRGP_TADGRLKPEVVAPGVDIIAPRASGTSNGTPIND---YYT 372
                                                                                                                                                                                                                                                                                                                                                                                198 GHCTHVASIAAGTGAASNGKYKSMAPGAKLAGIKVLGADGSGSISTIIKGVEWAVDNKDK 257
                                                                                                                                                                                                                                                               258 YGIKVINLSLGSSQSSDGTDALSQAVNN-AMDAGIVYCVAAGNSGPNTYTVGSPAAASKV 316
                                                                                                                                                                                                                                                                                      373 KASGISMATPHVSGVGALIZGAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 KALQQTVIADPVSVSFGVQQWPHIDDEPVTKQLTYRNLGTQDVTLKLISTATDPKGKAAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AGFFTLGATTVTVPA---GGSASVDMTADTRLGGTVDGAYSAYVVATGGGTVRTAAAVQ 406
                                                                                     138 IDESAAQVMATYVWNLGYDGSGITIGIIDTGIDASHPDLQGKVIGWVDFVNGRSYPYDDH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 VKVVSY-------KGAA@YQVDVVSDGSLSQSGGGNPNPNPNPNPTPTTDTQTF-- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 REVESYDVIVRHIGRDGKPITEHLIDLIGYAGLGSGRGYG-----APAIDIATLRL 457
                                                 Gaps
                                                                                                                 233 TISGISMATPHVAGAAALLKQOHPDWISAELKGAL--TGSTKGGK-YTPPEQGSGRIQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 KAIK-----YDDYAKLTFTGSVADKGSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 HTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAGTWT
                                               79;
                                            55; Mismatches 183; Indels
    DB 18;
Score 679.5;
Pred. No. 3.96
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Job time : 33 secs
    19.8%
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    Query Match
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This sequence is a fragment of an asymmetric hydrolase which acts one 4-substituted-1,4-dihydropyridine derivatives. The DNA sequence encoding the hydrolase (DhpA) was isolated from the chromosomal DNA of Streptomyces viidosporus. The enzyme allows the efficient conversion of 4-substituted-1,4-dihydropyridine esters to chiral partially hydrolysed derivatives, for use in the synthesis of cardiovascular drugs

us-09-841-553-5.rai

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-841-553-5 3428 1 MKGLKALILUVLGLVVGS........YAYSTYGHADYQLKAVVYYG 659

Scoring table:

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

231628 seqs, 24425594 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Winimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA;*

1. /cgnz_6/ptodata_1/1.aa_/5A_COMB.pep:*

2. /cgnz_6/ptodata_1/1.aa_/5B_COMB.pep:*

3. /cgnz_6/ptodata_1/1.aa_/6A_COMB.pep:*

4. /cgnz_6/ptodata_1/1.aa_/6A_COMB.pep:*

5. /cgnz_6/ptodata_1/1.taa_FCTUS_COMB.pep:*

6. /cgnz_6/ptodata_1/1.taa_FCTUS_COMB.pep:*

6. /cgnz_6/ptodata_1/1.taa_FCTUS_COMB.pep:* Database:

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result boing printed, and is derived by analysis of the total score distribution.

STHAMMUS

Result Query Description No. Score Match Length DB ID 13428 100.0 659 4 US-08-894-818B-5 Sequence: 5, Appliance: 6, Ap			æ			SUMMARIES	w To To
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28 543.5 15.9 352.17 US-07-921-260A-2 29 543 15.8 392.1 US-08-460-343B-2 31 540 15.8 392.1 US-08-460-343B-2 32 540.5 15.8 1398 1 US-08-504-265B-2 34 540.5 15.8 1398 4 US-08-750-532-9 35 537.5 15.7 350 1 US-08-48-418B-8 36 537.5 15.7 360 3 US-09-049-8 37.5 15.7 360 3 US-09-049-8 38 537.5 15.7 360 4 US-08-265-050-2 38 537.5 15.7 380 4 US-08-265-050-2 41 537.5 15.7 380 6 US-08-265-050-2 42 537.5 15.7 380 6 S21787B-2 43 535 15.7 380 6 S21787B-2 44 535 15.7 380 6 S21787B-2 45 537 15.7 380 6 S21787B-2 46 535 15.7 380 6 S21787B-2 47 537 15.7 380 6 S21787B-2 48 535 15.7 380 6 S21787B-2 48 535 15.7 380 6 S21787B-2 49 537 15.7 380 6 S21787B-2 40 537 15.7 380 6 S21787B-2 41 537 15.7 380 6 S21787B-2 42 537 15.7 380 6 S21787B-2 43 535 15.7 380 6 S21787B-2 44 535 15.7 380 6 S21787B-2 45 537 15.7 380 6 S216611-2	RESULT 1 US-08-894-8188-5 Sequence 5, Application Us/08894818B Patent No. 051822 GENERAL INFORMATION: APPLICANT MORISHITA, Mio APPLICANT MORISHITA, Mio APPLICANT MARAMOTO, Katsuhiko APPLICANT MARAMOTO, Katsuhiko APPLICANT ASADA, Kiyozo APPLICANT ASADA, Kiyozo APPLICANT ASADA, Kiyozo APPLICANT TSUNASAWA, Susumu APPLICANT ASADA, Kiyozo INVERTION: HYPERTHERWOSTABLE PROTEASE GENES CORRESPONDENCES: 42 CORRESEE: Broady and Melmark STREET: 419 Seventh Street N.W., Ste. 300 STREET: 419 Seventh Street N.W., Ste. 300	COUNTY: United States of America 210: 2004 COUNTY: United States of America 210: 2004 COMPUTER: READABLE FORM: 0.5 MEDIUM TYPE: Floppy disk COMPUTER: IBN PC COMPSTANDS CONTYER: THEN PC COMPSTANDS SOFTWARE: PATENTIN RELEASE 11.0, Version 11.30 CURRENT APPLICATION DATA: APPLICATION NUBER: US/08/094,818B FILING DATE: 20-MAY-1996 CLASSIFICATION NUBER: PCT/JP96/03253 PRIOR APPLICATION NUBER: PCT/JP96/03253 FILING DATE: 12-DEC-1995 ATTORNEY/AGENT INFORMATION REPERRICE/DOCKET NUMBER: 35,618 REFERENCE/DOCKET NUMB	i p

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                               Length 659;
                                                                Indels
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APPLICANT: WORISHITA, MAO
APPLICANT: WORISHITA, MAO
APPLICANT: MITTA, MASANOT, KATSHIKO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: TSUNASANA, SUSUMU
APPLICANT: KATO, IKUNOShin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS: 42
CORRESPONDENCE ADDRESS: 42
ADDRESSEE: Browdy and Neimark
STREET: A19 SEVENTH STREET N.W., Ste. 300
                               100.0%; Score 342%; DB 4;
100.0%; Pred. No. 1.1e-241;
ive 0; Mismatches 0;
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                                                   Best Local Similarity 100.
Matches 659; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISTIIKGVEMAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 TSMGTPINDYYIKASGISMARRYSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIAYGAGRVNVYKAIKYDDYAKLIFIGSVADKGSATHTFDVSGATFVTATLYMDTGSSDI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TVIVFENHREKEIAVRVLULÄGAKVRYVYHIIPAIAADLKVRDLLVISGLTGGKAKLSGV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; DB 4;
5e-210;
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC COMPS.LIDE
CORPUTER: ISM PC COMPS.LIDE
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.4%; Score 2997.5;
88.3%; Pred. No. 2.5e
Live ()2; Mismatches
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,/8/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 20-MAY-1998
FILING DATE: 07-NOV-1996
FILING DATE: 07-NOV-1996
APPLICATION NUMBER: JP 33285/1995
ATTORRY/AGENT INFORMATION!
NAME: BIOWAY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                    KEGISTRATION NUMBER: 25:618
REPERENCE, DOCKET NUMBER: TAKAKURA-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                    TELERAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHRANCTERISTICS:
LENTH: 654 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.39
Matches 582; Conservative
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601 LDLYLYDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLVYAYSTYGWADYQLKAVVYYG 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 NTRVSGIKFLQEDVKVQVDCA----TSVSQIGADTVMNSLGYDGSGVVVALVDTGLDAN 173
                         1 MKGLKALILVILVLGLVYGSVAAAPEKKVEQVRN---VEKNYGLLTPGLFRKIQKLNPNE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 85.0%; Score 2914; DB 4; Length 659; Best Local Similarity 83.7%; Pred. No. 3e-204; Matches 558; Conservative, 47; Mismatches 46; Indels 1
                                                                                                                                                                                                   APPLICANT: TAKAGUA, HIKARU
APPLICANT: TAKAGUA, HIKARU
APPLICANT: YAMAMOTO, Kācsuhiko
APPLICANT: YAMAMOTO, Kācsuhiko
APPLICANT: ASADA, KIYOZO.
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: KATO, IKUNOShin
TILE OF INVENTION: KYPEKTHERNOSTABLE PROTEASE GENES
CORRESPONDENCE ALDRESS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Browdy and Netmark
STREET: 419 Seventh Street N.W., Ste.
LITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSICCATION: 435

RIOR APPLICATION DATA:
APPLICATION NUMBER: PST/JP96/03253
FILING DATE: 07-NOV-1955
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.C. United States of America
                                                                                                                                            Sequence 1, Application US/08894818B Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-8188-1
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MEDIUM TYPE: Floppy
                                                                                                                                                                                        GENERAL INFORMATION:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Sequence 3, Application US/08894818B ; Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T: MORISHITA, Mic
T: YAMAMOTO, Karëshliko
T: MITTA, Masenori
T: ASADA, Kiyozo
T: TSUNASANA, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKAKURA, Hikaru
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STATE: D.C.
COUNTRY: United St
ZIP: 20004
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                               HPDLQGKVIGWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKV 232
                                            LGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV 292
                                                                                                                                           VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                            193 YCVAAGNSGPUTYTYGSPAAASKYITYGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                                                                                                                                   IVAPKEIADIAYGAGRVNYYKAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLY 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 WDTGSSDIDLYLYDPNGNEYDYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDV 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TAKAKUBA, HIKATU
APPLICANT: THOORISTITA, Mio
APPLICANT: SHIMONO, TOOMOKO
APPLICANT: SADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVERTION SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKUBA-6
CURRENT APPLICATION NUMBER: 15999-12-06
PRIOR APPLICATION NUMBER: 15999-12-06
PRIOR FILING DATE: 1997-06-10
NUMBER OF PSQ ID NOS: 33
SOFTWARE: PATENTIN VEISION 3.0
SEQ ID NO 12
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tes 46; Indels 10
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85.0%; Score 2914; DB
Best Local Similarity 83.7%; Pred. No. 3e-20
Matches 558; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 12, Application US/09445472
; Patent No. 6358726
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TYPE: PRT
ORGANISM: Thermococcus celer
US-09-445-472-12
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533 VSDGSLSDSGGGNPNPNPNPNPNPTIDIQTFTGSVNDYWDTSDTFTMNVNSGATKITGDL 592
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                                                                                                        292
                                                                                                                        293 VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                        IVAPKEIADIAYGAGRVNVYKAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLY
                                          173 HPDLQGKVIGWVDFVNGRSYPTDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKV
                                                            233 LGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KATO, IKUNOSÄIN
TITLE OF INVENTION: HYPERTHERWOSTABLE PROTEASE GENES
TITLE OF INVENTION: HYPERTHERWOSTABLE PROTEASE GENES
CORRESPONDENCES: 42
CORRESPONDENCES: ADDRESSE: Broady and Melmark
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER: READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING STETE: PC-DOS/MS-DOS
OPERATING STETE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
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133 ABLEGLDESAAQVMATYVWNIGYDGSGITIGIIDTGIDASHPDLOGKVIGWVDFVNGRSY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 PYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKYLGADGSGSISTIIKGVEWAV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 ASKVITVGAVDSNDNIASPSSRGPTADGRLKPEVVAPGVDIIAPHASGTSMGTPINDYYT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 KASGISMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAIKYDDYAKLTETGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEV 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 NPTPTTDTQTFTGSVNDY#DJSDTFTMNVNSGATKITGDLTFDTSYNOLDLYLYDPNGNL 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÿ
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590-60-61, Application US-09445472
5940-60-61, Application US-09445472
5940-60-61, Application US-09445472
5940-61, Patent No. 6358726
5940-61, Patent No. 6358726
5940-61, Patent No. 6358726
5940-61, Patent Norishita, Missaphita Sahoa, Missaphita Natura Sahoa, Missaphita S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.5%; Score 2349.5; DB 4; Length 522; Best Local Similarity 85.2%; Pred. No. 2.7e-163; Matches 449; Conservative 22; Mismatches 51; Indels 5;
APPLICANT: KATO, IKUNCEHÎN
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKKURA-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997;
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOCTWARE: PALENLIN VETSION 3:0
SEQ ID NO: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613 VDRSTSSNSYEHVEYAHPAPGTWTFLYYAYSTYGWADYQLKAVYYYG 659
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (428)...(428)
OTHER INFORMATION: Xaa at position 428 is Gly or Val.,
US-09-445-472-4
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pyrococcus furrôsus
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                       121 DNKDKYGIKVINLSLGSSQSSDGTDALSQAVNAAWDAGLVVVVAAGNSGPNKYTIGSPAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 68.5%; Score 2349.5; DB 4; Length 522; Best Local Similarity 85.2%; Pred. No. 2.7e-163; Matches 449; Conservative 22; Mismatches 51; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTHER INFORMATION: /note= Xaa at position 428 is Gly or Val
US-08-894-818B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/JP96/03253
FILIGO BATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: JP 323285/1995
FILIGO BATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BLOWDY, ROGER L.
RECERRACE/DOCKET NUMBER: 25.618
REFERENCE/DOCKET NUMBER: TAKKURA-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 antino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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PARENT NO. VA-VA-TON.

GENERAL INFORMATION:

APPLICANT: Akira ARISAWA et al.

TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC

TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE

TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE

TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE

TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DE

TITLE OF INVENTION: HYDROLASE ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTIVITY FOR ACTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 ADGSGSISTIIKGVEWAVDNZDKTGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIYVC 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1045.5; DB 1;
Pred, No. 8e-69;
9; Mismatches 19;
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: MR COMPATIBLE
COMPUTER: MR COMPATIBLE
COMPUTER: MR COMPATIBLE
COMPATING SYSTEM: MS-DOS
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APPLICATION NUMBER: JP 1994/130236
FILING DATE: 13-010-1994
PRICATION NUMBER: JP 1994/13912
FILING DATE: 26-010-1994
ATTORNEYAGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: Z5,618
REFERENCE/DOCKET NUMBER: MITTA-1
TELEPHONE: (202) 528-5397
TELEPHONE: (202) 528-5397
TELEPHONE: (202) 528-5397
TELEPHONE: (202) 528-5397
TELEPHONE: (202) 528-5397
TELEPHONE: (202) 528-5397
TELEPHONE: (202) 737-3528
INFORMATION FOR SED ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids;
TYPE: amino acids
STANDENLESS: single
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/0900016 Patent No. 6143541
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Best Local Similarity 87 4%;
Matches 202; Conservative
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APPLICANT: MITTA, MASANORI
APPLICANT: MITTA, MASANORI
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADO, IKUNOSHINI
APPLICANT: TATU, IKUNOSHINI
TITLE OF INVENTION: HYPERTHERNOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE PORN:
MEDIOM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
OFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: Us/08/750,532
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.5%; Pred. No. 5.1e-132;
Matches 367; Conservative 15; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Suite 300 CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
           CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08750532 Patent No. 5756339
                                                                                                                                                 SEQ ID NO 1
LENGTH: 412
TYPE: PRT
SORGANISM: Pyrococcus furiosus
US-09-445-472-1
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TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE ITS FAPRESSION PRODUCT CORRESPONDENCES 7

CORRESPONDENCE ADDRESS.
ADDRESSEE: Wenderath Symptom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ' 110 LTGGKAKLSGVRFIQEDYKYTVSAELEGLDESAADVMATYVWNLGYDGSGITIGIIDTGI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 DASHPDLQGKVIGWVDFWWGRSYPYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 APGVDIIAPRASGTSMGTPIND---YYTKASGTSMATPHVSGVGALILQAHPSWTPDKVK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30,2%; Score 692.5; DB 4; Length 823; Best Local Similarity 33,6%; Pred. No. 2.38-42; Matches 202; Conservative 62; Mismatches 223; Indels 115; Gaps
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                                                                                                                                                                     ADDRESSE: Wenderch, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Weahington
STATE: D.C.
COUNTRY: U.S.A.
2.P: 20006
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Competible
COMPUTER: Wordperfect, 5.05
SOFTWARE: Wordperfect, 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,016
FILING DATE: January 30, 1998
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 TALIETADIVAPKEIADIAXGAGRVNVYKAIK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warren M. Cheek, Jr.
RECISTRATION NUMBER: 33,367
REFERENCE/COCKET WUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 823 amino acida TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-09-000-016-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-721-826
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 GNEVDYSTTAYYGFEKVGYXNPTAGTWTVKVVSY------KGAANYQVDVVSDGS 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 GGTVDGAYSAYVVATGGGGTVRTAAAVQREVESYDVTVRHIGRDGKPTTEHLTDLIGYAG 642
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; Pred, No. 2e-42;
62; Mismatches 223; Indels 115; Gaps
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US-09-000-016-2
; Sequence 2, Application US/09000016
; Patent No. 6143341
; GENERAL INFORMATION:
                                                          APPLICATION NUMBER:
FILLM DATE:
ATTORNEY/ACBNT INFORMATION:
NAME: Warren M Check, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/OCCKET NUMBER:
TELEPHONE: 202-721-8200
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 smino acida
TYPE: amino acid
STRANDEDNESS: aingle
TOPOLOGY: linear
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Best Local Similarity 33.6%;
Matches 202; Conservative 63
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MOLECULE TYPE: protein
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258 YGIKVINLSLGSSQSSDGTGSLSQAVNN-AWDAGIVVCVAAGNSGPNTYTVGSPAAASKV 316
                                                                    290 KALQQTVIADPVSVSFGVQQWPHTDDEPVTKQLTYRNLGTQDVTLKLTSTATDPKGKAAP 349
                                                                                                                                                                                                                                                                                                                                                                                       457 HTFDVSGATEVTATLYWDTGSSDIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAGTWT 516
                                                                                                                                                                                                                                                                                                                                                                                                                             350 AGFFILGATIVIPA -- GĞSASVDMTADTRLGGTVDGAYSAYVVATGGGQTVRTAAAVQ 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 REVESYDVTVRHIGRDGKPTTBHLTDLIGYAGLGSGRGYG------APATDTATLRL 457
60 GHGTHVASTAAGTGAQSKGKYKGVAPGAAILNGKVLDDSGFGDDSGILAGMEWAA----A 115
                                                                                                                            317 ITVGAVDSNDNIASFSSRGP-TADGRLKPEVVAPGVDIIAPRASGTSMGTPIND---YYT 372
                                                                                                                                                                                                                   373 KASGISMAIPHVSGVGALILQAHPSWIPDKVKIALIETADIVAPKEIADIAYGAGRVNVY 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 VKVVSY-----KGAANYQVDVVSDGSLSQSGGCNPNPNPNPNPTPTTDTQTF-- 563
                                                                                                                                                                                                                                                                                                     ----YDDYAKLTFTGSVADKGSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/OR685774
Fatent No. 5712147
Fatent No. 57121470:
GENERAL INFORMATION:
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Lin, Xiang
APPLICANT: Hiler, Eric S.
TITLE OF INVENTION: PND-1 KERATINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
COUNTRY: Use 1.28234
ZIP: 28234
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: SAFTEM: PC-D3/MS-D0S
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/08/685,774
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/250,028,
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: SIDICY, Kenneth,D.
REGISTRATION NUMBER: 341,665
REFERENCE/DOCKET WOMBER; 506
REFERENCE/TOCKET NUMBER; 507
TELECOMMUNICATION: (919) 420-2203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 -TGS-VNDYWDTSDTFTM 579
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INFORMATION FOR SEQ ID NC: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids:
                                                                                                                                                                                                                                                                                                       433 KAIK-----
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TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC FOR THE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIVITIE OF INVENTION: ITS EXPRESSION PRODUCT
                                                                                                                                                                                                       AKPLSAT --- IGYTYDT 73F
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                                   ----KGAANYQVDVVSDGS 537
                                                                                                                          643 LGSGRĞYG------APATDTATLELPKGTYLVDSWIAKDFGTLKGGIDWLVQPKLSV 693
                                                                                                                                                                           586 TKITGDLIPDT-SYNDLDLYLYDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLVYAYST 644
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55; Mismatches 183; Indels
                                                                                         538 LSQSGGGNPNPNPNPNPTPTDTQTF---TGS-VNDYWDTSDTFTM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FRADABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inch, 1.44 mb
COMPUTER: DISKETCH: 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,016
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCESS:
ADDRESSEE: Wenderoch, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CLTY: Weshington
STATE: D.C.
COUNTRY: U.S.A.
    189 GNEVDYSYTAYYGFEKVGYYNPIAGTWTVKVVSY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.8%; Score 679.5; 36.3%; Pred. No. 1.1s
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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMEER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPRONUNICATION INFORMATION:
TELEPRONE: 202-721-8200
TELEPRONE: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                  645 YG 646
                                                                                                                                                                                                                                                                                                            732 AG 733
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US-09-000-016-7
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288 DAGIVYCVAAGNSGP--NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPE 345
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                                                                                                                                                                                                                                                                    57 ERISTVIVEENHREKEIÄVR --- VLELMGAKVRYVYHIIPAIAADLK--- VRDLLVISGL 110
                                                                                                                                                                                    111 TGGKAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGID 170
                                                                                                                                                                                                                                                171 ASHPDLQGKVIGWVDFVNGRSYPY-DDHGHGTHVASIAAGTGAASNGK--YKGMAPGAKL 227
                                                                                                                                                                                                                                                                                                            228 AGIKVLGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAW 287
                                                                                                                                                      41 -----IVGEKQIMSIMSAAKKKDVISEKGGKVQKQFKYVDAASATLNEKAVKEL----- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HSIAO, Humg-Yu
APPLICANT: FONCE, Douglas W.
APPLICANT: LALGNDE, James J.
TITLE OF INVENTION: ALFALINE PROTEASES STABLE IN HEAVY-DUTY
TITLE OF INVENTION: DETERGENT LIQUIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy dlak
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/772.087
16754/115 CHCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLENTT----TKLGDSFYKGKGLINVQAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 ALIETADIVAPKEIAD-IAYGAGRVNVYKA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/07772087 Patent No. 5275945 GENERAL INFORMATION:
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & L
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STATE: Virginia
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CLASSIFICATION:
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US-07-772-087-4
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                                                                                                                                                                                                                                                                                                         63 IVFENH-REKEIAVRVLELMGAKVRYVYHIIPAIAADLKVRDLLVISGLTGGKAKLSGVR 121
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                                                                                                                                                                                 ; Score 557; DB 1; Length 379; Pred. No. 5.78-33; 62; Mismatches 148; Indels 74;
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16.2%; Score 555; DB 4; Length 38; Best Local Similarity 35.1%; Pred. No. 8.1e-33; Matches 158; Conservative 65; Mismatches 141; Indels
                                                                                                STRAIN: PWD-1
US-08-685-774-2
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Patent No. 6358726
GENERAL INFORMATION:
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US-09-445-472-31
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241 ISTIIKGVEMAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNS 300
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                                                                                                                                                                                                                                                                                                                                                                                      183 WVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGK--YKGMAPGAKLAGIKVLGADGSGS 240
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                                                                                                                           Indels
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                                                                                          Query Match
Best Local Similarity 34.2'
Matches 149; Conservative
                                     Carlaberg
; ORIGINAL SOURCE:
; ORGANISM: Bacil;
; STRAIN: Carlybe
US-07-772-087-4
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